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Risk Analysis of Disease Transmission between Domestic Sheep and Goats and Rocky Mountain Bighorn Sheep

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Acronyms and Abbreviations

BIA – Bureau of Indian Affairs
BLM – Bureau of Land Management
BTNF – Bridger-Teton National Forest
CFR – Code of Federal Regulations
FSM – Forest Service Manual
KCS -- keratoconjunctivitis
MOU – Memorandum of Understanding
NEPA – National Environmental Policy Act
NFMA – National Forest Management Act
NFS – National Forest System
RADT – Risk Assessment of Disease Transmission
SNF – Shoshone National Forest
WGFD – Wyoming Game and Fish Department

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Background

The 1982 planning regulations (36 CFR 219.19) that interpreted the National Forest Management Act (NFMA) imposed requirements that forest plans include provisions to manage habitats to support viable populations of native and desired non-native vertebrate species on national forests and grasslands. For planning purposes, a viable population is regarded as one that has the estimated numbers and distribution of reproductive individuals to ensure its continued existence is well distributed in the planning area.

Rocky Mountain bighorn sheep (*Ovis canadensis*) are designated by the Forest Service Rocky Mountain Region (Region 2) as a sensitive species on National Forest System lands within the Region (USDA Forest Service 2017a). The sensitive species designation implies there is concern for the long-term viability and/or conservation status of bighorn sheep on National Forest System (NFS) lands in the Region (Forest Service Manual 2670.5, Beecham et. al 2007). For this reason, Forest Service Manual (FSM) sections 2670.32 and 2672.1 direct the National Forests to avoid or minimize impacts to species listed by the Regional Forester as a sensitive species. The Shoshone National Forest (SNF) supports one of the largest metapopulations of bighorn sheep in the lower 48 (the Absaroka metapopulation). On a statewide basis, the SNF is key to maintaining bighorn sheep in Wyoming (McWhirter, WGFD, pers. comm. 2017).

Although habitat degradation from fire suppression, highways, non-native invasive weeds, and human disturbance are also concerns, the susceptibility of bighorn sheep to population declines or extirpation due to respiratory diseases, which can be transmitted by domestic sheep or goats (Besser et al. 2012b, Cassirer et al. 2013), is the greatest concern for bighorn sheep on the SNF. Therefore, analyzing and disclosing the potential effects of domestic sheep, domestic goat, and pack goat use on bighorn sheep is needed to meet Forest Service direction for sensitive species management, as described in FSM 2672.4.

In order to maintain viable populations of bighorn sheep on the SNF, there must be sufficient habitat where there is not a substantial risk for disease transmission from domestic sheep and goats. In effect, areas of domestic sheep and goat use can create “sink” habitats – habitats that are otherwise suitable for bighorn sheep, but in which bighorn sheep populations may be subject to disease transmission from domestics. In addition, once disease is introduced into bighorn sheep populations, they can transmit these diseases to other wild sheep populations. As a result, identifying areas of domestic sheep and goat use that pose a risk of interspecies contact and disease transmission, and identifying options to reduce this risk, are key aspects of bighorn sheep management on National Forests. The term “disease transmission” as used in this report, refers to a process where pathogens are transmitted from one animal to another, with the subsequent development of disease symptoms.

In addition to direction provided in FSM 2670, the Forest Service Washington Office has issued several letters regarding bighorn sheep analysis for National Environmental Policy Act (NEPA) documents, which form the basis of this Risk Assessment for Disease Transmission (RADT). An August 2011 letter from the Deputy Chief of the Forest Service directs National Forest units considering projects with the potential for physical contact between bighorn and domestic sheep, with subsequent potential for disease transmission, to conduct a Risk Assessment analysis. The letter states “Forests that have necessary data, issue complexity, and the ability to conduct a quantitative bighorn sheep viability analysis may do so.

However, a qualitative approach to NEPA analysis for bighorn sheep viability is sufficient as long as clear and reasonable rationale for the decision is displayed" (USDA Forest Service 2011).

Subsequent guidance letters were provided to (1) describe availability of products to accomplish the first two steps of the process (USDA Forest Service 2012b), and (2) clarify the role of best management practices in the overall balance of multiple-use demands and management practices to support viable populations (USDA Forest Service 2014). Although the 2011 guidance letter focused on bighorn sheep and domestic sheep, the 2012 letter expanded the approach to include domestic goat grazing. This RADT utilizes the process described in these guidance letters, with a qualitative approach to determine the risk of contact between bighorn and domestic sheep, domestic goats, and pack goats on the SNF (see *Methods* for the rationale).

The goal of this RADT is to assess the potential risk of physical contact between bighorn sheep and domestic sheep, domestic goats, and pack goats on the SNF and the subsequent possibility of disease transmission to bighorn sheep. This RADT has been developed on the basis of existing Forest Service direction, policy, and guidance and relies on the best available science regarding disease transmission and potential impacts to bighorn sheep, status of bighorn sheep on the SNF, and current information on domestic sheep, domestic goat, and pack goat use of the SNF. This RADT replaces the previous version developed in support of the SNF's 2015 Record of Decision for the Land Management Plan Revision.

This document uses several terms to define bighorn sheep occurrence. Bighorn sheep herd units are defined by the Wyoming Game and Fish Department (WGFD) using broad-scale delineations to identify different herds for management purposes. Core native bighorn sheep ranges is another term used for herd units that were delineated for core native bighorn sheep herds. Occupied habitat is a more refined depiction of habitat used by bighorn sheep within the herd unit boundary. Occupied habitat is identified by WGFD based on bighorn sheep location data and other local knowledge. Both occupied and unoccupied bighorn sheep habitat are included within herd unit boundaries. Bighorn sheep herd unit boundaries relative to occupied habitat are shown in Figure 2.

The Final Report and Recommendations from the Wyoming State-wide Bighorn/Domestic Sheep Interaction Working Group (2004a) is an important guidance document that was considered in this report. This Working Group includes Federal and State agencies, livestock producers, non-governmental organizations, and others with an interest in bighorn and domestic sheep management, and was initiated in response to concerns over bighorn and domestic sheep interactions. The group implemented a statewide approach to developing collaborative recommendations culminating in a final report in 2004. The recommendations included the need to minimize the risk of disease transmission, and to optimize preventive management procedures to ensure healthy populations of bighorn and domestic sheep. Additionally, the group mapped statewide bighorn sheep management areas and delineated them into core native herds, cooperative review areas, and bighorn sheep non-emphasis areas (Wyoming State-wide Bighorn/Domestic Sheep Interaction Working Group 2004b). Core native bighorn herds are those populations that have never been extirpated and repopulated. The group agreed that core native herds were the highest priority areas for bighorn sheep, where all efforts would be made to prevent contact between bighorn and domestic sheep within the Terms of Agreement put forth in the Wyoming Plan. Cooperative review areas encompass suitable bighorn sheep range where proposed changes in bighorn sheep

management or domestic sheep use will be cooperatively evaluated. A Master Memorandum of Understanding for the Management of Bighorn Sheep on National Forest System (NFS) Lands in Wyoming (2016) was signed in January of 2016 by the Forest Service Rocky Mountain Region and the Wyoming Game and Fish Department (WGFD). The purpose of this Memorandum of Understanding (MOU) is to document the cooperative efforts to manage bighorn sheep herds and their habitats on NFS lands in the State of Wyoming to be undertaken by WGFD and the Forest Service. Specifically, the parties agreed to collaborate to implement the "2004 Final Report and Recommendations from the Wyoming State-wide Bighorn/Domestic Sheep Interaction Working Group" on NFS lands.

Introduction

Historical Bighorn Sheep Distribution and Abundance

Bighorn sheep were once one of the most abundant wild ungulates in the West. Population estimates range from 1.5 million to 2 million at the onset of the 19th century (Lawrence et al. 2010, WAFWA 2012). Populations declined with the westward expansion of human populations due to overhunting, introduction of domestic sheep and goats, and overgrazing of rangelands. Bighorn populations began to decline dramatically in most areas about 1880. By 1900, many populations were eliminated (Buechner 1960).

Disease contributed to the decline of bighorn sheep populations (Beecham et al. 2007, CAST 2008), and many native herds declined to less than 10% of their historical size. According to historical accounts, such declines coincided with the advent of domestic livestock grazing on ranges occupied by bighorn sheep (Grinnell 1928, Schillinger 1937, CAST 2008). Epizootics among native bighorn herds were reported in various locations following European settlement and establishment of domestic livestock grazing, with reports from Colorado as early as 1885 (Coggins 2010). These observations may reflect the introduction of novel bacterial pathogens (including some strains of *Pasteurella* [*Mannheimia*] spp.) to naïve bighorn populations beginning in the late 1800s (Grinnell 1928, Marsh 1938).

By 1950, bighorn sheep were extirpated from a large portion of their range. Restoration and protection efforts have allowed populations of bighorn sheep to grow from an estimated 25,000 in 1955 (Buechner 1960) to 70,000 in the 1990s (Valdez and Krausman, 1999), but many extant populations of bighorn sheep consist of fewer than 100 individuals in a fragmented distribution across the landscape (Singer et. al 2000a). Even with ongoing recovery efforts, current bighorn sheep numbers in the Western United States are estimated to be less than 10% of pre-settlement populations (Schommer and Woolever 2001).

Rocky Mountain bighorn sheep are native to Wyoming and, historically, bighorns ranged across most of the state within suitable habitat. The SNF has the largest number of bighorn sheep of any National Forest within National Forest System lands, with about 4,550 of the 6,000 bighorn sheep in Wyoming (using 2016 estimates). Northwestern Wyoming contains eight core native bighorn sheep herds, which are herds that have never been extirpated and re-populated with transplanted bighorn sheep (Wyoming State-wide Bighorn/Domestic Sheep Interaction Working Group 2004a). These are Wyoming's largest and most robust bighorn sheep populations and are the highest priorities for bighorn sheep management in Wyoming (Wyoming State-wide Bighorn/Domestic Sheep Interaction Working Group 2004a). Core native herds include the Clarks Fork, Trout Peak, Wapiti Ridge, Younts Peak, Francs Peak,

Targhee, Jackson, and Whiskey Mountain Herds, which account for more than 90% of the bighorn sheep in the state. Two of these core native herds have suffered significant die-offs in the past due to bacterial pneumonia. The Jackson herd, on the Bridger-Teton National Forest (BTNF), experienced a significant die-off in 2002 and the Whiskey Mountain herd (SNF) has suffered through several outbreaks of the disease (WGFD 2017b). Managers also suspect that disease played a role in a population decline in the southern Absaroka Mountains during 2011–2013, which coincided with a particularly severe late-winter/spring in 2011 (McWhirter, WGFD, pers. comm., 2017).

Bacterial Pneumonia

The main obstacle to restoring bighorn sheep populations is polymicrobial bacterial pneumonia (George et al. 2008, Cahn et al. 2011), primarily bacteria of the family Pasteurellaceae (*Pasteurella multocida*, *Mannheimia haemolytica,* and *Bibersteinia trehalosi*), and *Mycoplasma ovipneumoniae* (Martin et al. 1996, Schommer and Woolever 2001, Herndon et al. 2011, Wood et al. 2017). The relative importance of these bacteria in the development of pneumonia in bighorn sheep is not clearly defined in the literature. The scientific literature recognizes this uncertainty. For example, Besser et al. (2012*b*) stated, "considering the dramatic and severe character of epizootic bighorn sheep pneumonia, the etiology is surprisingly unclear." Casirrer et al. (2013) offered that, "the disease has been recognized for at least 80 years, but debate continues over the identities and roles of causal agents." Plowright et al. (2013) stated that, "pneumonia in bighorn sheep continues to be one of the most poorly understood and intractable diseases that threatens wildlife in the United States and Canada."

During disease outbreaks in bighorn sheep, members of the genera *Mannheimia*, *Bibersteinia*, and *Pasteurella*, including *Mannheimia* (*Pasteurella*) *haemolytica*, *Bibersteinia* (*Pasteurella*) *trehalosi*, and *Pasteurella multocida*, have commonly been isolated from pneumonic lungs (Herndon et al. 2011, Wood et al. 2017). (It should be noted that the organism called *Pasteurella haemolytica* has been renamed *Mannheimia haemolytica*, but because much of the scientific literature uses the old nomenclature, the names should be considered synonymous). Of the numerous pathogens affecting bighorn sheep, *Mannheimia haemolytica* consistently causes fatal bronchopneumonia in bighorn sheep under natural and experimental conditions (Foreyt 1992a, Herndon et al. 2011). Garde et al. (2005) cited evidence indicating that *Bibersteinia trehalosi* and *Pasteurella multocida* may be more pathogenic than previously thought. Although much of the scientific literature regarding pneumonia in bighorn has focused on these bacteria as primary agents of disease, some investigators have cited evidence indicating that they are less important as causal agents of pneumonia than previously believed (Besser 2013).

Some recent studies have pointed to *Mycoplasma ovipneumoniae* as being the primary pathogen of concern in the development of pneumonia in bighorn sheep (Besser et al. 2008, Besser et al. 2012*a*, Besser et al 2012*b*). *Mycoplasma ovipneumoniae* has a host range limited to the subfamily *Caprinae* (primarily sheep and goats) (Nicholas et al. 2008) and is carried by domestic sheep and goats (Ayling and Nicholas 2007). When *M*. *ovipneumoniae* is introduced into naïve bighorn sheep populations, outbreaks of polymicrobial pneumonia may ensue, sometimes resulting in high mortality in all age classes (Besser et al. 2008, 2014). *Mycoplasma ovipneumoniae* binds respiratory cilia, interfering with mucociliary clearance and facilitating infection by other bacteria species that leads to development of pneumonia

(Besser et al. 2013). Recent advances in diagnostic techniques have allowed more reliable detection of *Mycoplasma ovipneumoniae,* which has led to increasing awareness of this species' role in bighorn sheep pneumonia. Besser et al. (2008) analyzed diagnostic specimens taken from nine pneumonic bighorn sheep and *M. ovipneumoniae* was detected as a predominant member of the pneumonic flora in lambs with early lesions of bronchopneumonia. *M. ovipneumoniae* was the only agent detected at significantly higher prevalence in animals from outbreaks than in animals from unaffected healthy populations, and was the most consistently detected agent within each outbreak (Besser et al. 2012b). In a synthesis of the current state of bighorn sheep pneumonia, Cassirer et al. (2017) stated that "over time, paradigms of disease etiology have shifted…suspected causes have ranged from lungworm infection to leukotoxin positive Pasteurellaceae, to a multi-factorial respiratory disease complex", and concluded that *Mycoplasma ovipneumoniae* "currently represents the most parsimonious and well-supported model for a primary agent of bighorn sheep respiratory disease." However, they also recognized the need for further research on the role of co-infection by other pathogens as well as other factors affecting transmission, carriage, and immunity.

These data provide evidence that *M. ovipneumoniae* plays a primary role in the cause of widespread pneumonia in bighorn sheep. However, some recent studies have continued to show other bacterial species playing an important role in the development of pneumonia. For example, Wood et al. (2017) found lesions typical of pasteurellosis predominated in early lamb mortality from pneumonia in their study of wild bighorn sheep that had been removed to a captive setting. *Bibersteinia trehalosi* and *Pasteurella multocida* were identified as important contributors to the observed mortality. They concluded that pneumonia is a polymicrobial disease, and that a combination of pathogens is most significant at the herd level (Wood et al. 2017). Lawrence et al. (2010) stated that they believed only less-virulent strains of *Mannheimia haemolytica* required infection with *M. ovipneumoniae* or other predisposing agents in order to cause pneumonia, and that some strains of *Mannheimia haemolytica* could cause highly lethal forms of the disease to develop in the absence of *M. ovipneumoniae.* Besser et al. (2013) cited evidence for *Pasteurella multocida* playing an important role in bighorn sheep pneumonia, yet pointed out the uncertainty involved give that this species has received relatively little research attention.

In some bighorn epidemics, other endemic respiratory pathogens including parainfluenza-3 (PI-3) virus, respiratory syncytial viruses (RSV), and lungworms (*Protostrongylus* spp.) are also believed to have contributed to disease (Rudolph et al. 2007; Spraker et al. 1986).

The interaction of disease outbreaks in bighorn sheep populations with other stressors (both disease and otherwise) is poorly understood. Recent research suggests that the complex interactions of disease agents themselves increases uncertainty in diagnosis and may also predispose bighorn sheep to secondary disease events (Cassirer et al. 2016). Additional research is needed on the interactions of disease pathogens, but it is reasonable to expect bighorn sheep are susceptible to diseases caused by multiple pathogens that result in multiple disease cycles. Additional stressors, which can reduce the resistance of bighorn sheep to disease organisms, include overcrowding on limited range; harassment by dogs; encroachment by humans; heavy snowfall and other weather events (Bunch et al. 1999); poor nutrition; predation; other human disturbances such as roads, habitat degradation, and noise; breeding behavior; and the presence of other wildlife (Festa-Bianchet 1988, Foreyt 1989, Monello et al. 2001, Garde et al. 2005).

Behavioral Influences on Disease Transmission

Mannheimia spp. and *Pasteurella* spp. transmission both require direct or close (less than 60 feet) contact to transfer contagions through coughing or sneezing (Ward et al. 1997, Dixon et al. 2002, Lawrence et al. 2010). Similarly, *Mycoplasma ovipneumoniae* is transmissible by direct contact or aerosol (Garde et al. 2005), potentially over distances of tens of meters (Heinse et al. 2016). Although nose-to-nose contact is not required and aerosol transmission can occur, close contact is needed for transmission of these pathogens.

Bighorn sheep make occasional long-distance exploratory movements beyond their core home range (Singer et al. 2001, O'Brien et al. 2014). Singer et al. (2001) called these movements forays, and defined them as any short-term movement of an animal away from, and back to, its herd's core home range. This life-history trait may place bighorn sheep at risk of contact with domestic sheep and goats. The risk of contact between foraying bighorn sheep (mostly rams) and domestic sheep, domestic goats, or pack goats is related to the extent of bighorn sheep source habitat, proximity to domestic sheep or goats, distance of bighorn forays outside their core home range, and the frequency of bighorn forays outside their core home range.

The foray behavior of wild sheep, where individuals can travel up to 50 km, potentially facilitates the spread of disease (O'Brien et al. 2014). Survivors of disease outbreaks become carriers of the disease and serve as a source of infection for other animals in the same herd, or other populations, through natural movements, forays, or translocations. Domestic sheep, domestic goats, or pack goats may also stray and increase the potential for interaction. When forays result in contact with domestic sheep or goats, there is the potential for disease transmission to bighorn sheep that in turn can be transmitted to bighorn sheep.

Because disease events in bighorn populations often have severe repercussions that can last for decades, an understanding of bighorn forays is instructive for addressing the potential risks of interspecies contact. Data analyzed for the Hells Canyon bighorn population in Idaho found that 14.1% of rams and 1.5% of ewes forayed during the summer months (O'Brien et al. 2014). Of rams that made forays, 50% traveled at least 8.1 km and 10% of foraying rams traveled 21.7 km beyond their home range boundaries. However, forays exceeding 50 km have been documented (O'Brien et al. 2014).

Several studies have reported contact between bighorn sheep and domestic sheep (Ward et al. 1997, Dubay et al. 2002, Drew et al. 2014) and goats (Rudolph 2003, Drew et al. 2014, see photo from Heinse et al. 2016). Evidence indicates that bighorn sheep and domestic sheep, or bighorn sheep and domestic goats, are attracted to each other which increases the probability that they will make the close contact necessary for disease transmission. Drew et al. (2014) found that contact between bighorn sheep and domestic sheep and goats was weakly associated with the bighorn sheep rut and estrus in domestic species, and did not appear to be associated with foraging. They explained the contact between bighorn sheep and domestic sheep and goats reported in their study by stating that bighorn sheep are sociable animals that wander and seek association with domestic species. Wehausen et al. (2011) and Foreyt and Lagerquist (1996) both observed that the lack of disease transmission observed between bighorn sheep and wild and domestic animal species other than sheep and goats was better explained by interspecific behavioral patterns (i.e. lack of social attraction)

that largely preclude contact and disease transmission, rather than an implication that other species do not carry pathogens that can cause pneumonia in bighorn sheep.

Evidence for Disease Transmission from Domestic Sheep

Bighorn sheep are closely related to domestic sheep but did not evolve with them, and thus are more vulnerable to many infectious diseases commonly carried by domestic sheep, particularly to *M. haemolytica* (Jessup and Boyce 1993). In contrast, domestic sheep, originally from Europe, have evolved resistance to several forms of respiratory diseases and are often able to carry the disease-causing bacteria without clinical symptoms (Foreyt et al. 1994, George et al. 2008, Besser et al. 2012a, b; WAFWA 2012, Cassirer et al. 2013). Several studies have shown that these bacteria are highly virulent in wild bighorn sheep and prove lethal after transmission from domestic sheep herds (Foreyt et al. 1994, Beecham et al. 2007, Lawrence et al. 2010, Herndon et al. 2011, Besser et al. 2012b).

A large body of evidence underscores the risk of disease transmission from domestic sheep (e.g., Foreyt and Jessup 1982, Onderka and Wishart 1984, Jessup 1985, Black et al.1988, Coggins 1988, Festa-Bianchet 1988, Callan et al.1991, Coggins and Matthews 1992, Foreyt 1994, Martin et al. 1996, Coggins 2002, George et al. 2008, Jeffress 2008, Lawrence et al. 2010, Miller et al. 2011, 2012; Besser et al. 2012a, WAFWA 2012) to wild sheep. The literature includes both circumstantial evidence linking bighorn die-offs in the wild to contact with domestic sheep, and controlled experiments where healthy bighorn sheep exposed to domestic sheep subsequently displayed high mortality rates (e.g., Goodson 1982, Foreyt 1989, 1990, 1992a, b, 1994; Foreyt et al. 1994; Onderka et al. 1988; Onderka and Wishart 1988; Garde et al. 2005, Lawrence et al. 2010, Drew et al. 2014).

Experiments

Controlled research studies have confirmed that both *Mannheimia hemolytica* and *Mycoplasma ovipneumoniae* can be transmitted to wild sheep upon contact with, or proximity to, domestic sheep (Lawrence et al. 2010, Wehausen et al. 2011, Besser et al. 2014). Domestic sheep commonly carry these disease-causing organisms, which typically cause few deaths and little illness in domesticated adults and lambs (Martin et al. 1996, Gilmour and Gilmour 1989). Numerous controlled experiments have shown more than 90% mortality in bighorn populations due to respiratory diseases within 2 months after exposure to domestic sheep (Foreyt 1989, Onderka and Wishart 1988, Drew et al. 2014). Co-mingling of domestic sheep and bighorn sheep under experimental conditions unequivocally results in transmission of bacterial pneumonia (*Mannheimia haemolytica*) from domestic sheep to bighorn sheep (Lawrence et al. 2010). Several co-pasturing studies revealed that 40 of 42 (95%) bighorn sheep died from pneumonia after association with domestic sheep (Foreyt 1995). All domestic sheep remained healthy. Supporting these observations, more than 95% of 90 bighorn sheep in 11 independent accidental (N=2) or experimental (N=9) studies involving contact with domestic sheep suffered fatal pneumonia within 100 days (Besser et al. 2012a).

Field Evidence of Large-scale, Rapid, All-age Die-offs

Pen experiments cannot by themselves determine whether transmission of fatal disease between domestic sheep and bighorn sheep actually occurs in the wild. Given the evidence

from pen experiments, it is likely that transmission of pneumophilic bacteria could also occur in the wild.

Disease-caused mortality events have been recorded in wild populations immediately after contact with domestic sheep in Oregon, Colorado, Washington, California, Nevada, Montana, the Dakotas, British Columbia, Alberta, and other locations (Foreyt and Jessup 1982, Onderka and Wishart 1984, Coggins 1988, Foreyt 1989, Callan et al. 1991, Garde et al. 2005, George et al. 2008). Martin et al. (1996) summarized more than 30 published cases where bighorn die-offs are believed to have resulted from contact with domestic sheep. In most cases, from 75 to 100% of the bighorn herd died. Domestic sheep always remained healthy. In 1997 in Colorado, George et al. (2008) observed a single domestic ram grazing with a group of bighorn sheep, 14 km from the nearest herd of domestic sheep. It was the first and only time during their 10-year study that the authors saw domestic sheep with bighorn sheep, and it coincided with the beginning of a disease outbreak that eventually spread to two additional herds.

These observations are consistent with the hypothesis that disease transmitted by domestic sheep cause die-offs of bighorn sheep herds. With one possible exception, no studies report any bighorn sheep herds, fenced or free ranging, that have come into contact with domestic sheep and remained healthy (Schommer and Woolever 2001). That exception was Besser et al. (2012*a*), which reported that three of four bighorn sheep survived for >100 days after being co-mingled with domestic sheep testing negative for *Mycoplasma ovipneumoniae* (the fourth bighorn sheep died of acute pneumonia). When contact between bighorn sheep and domestic sheep is documented, the severity of the bighorn sheep die-off is typically greater (Onderka and Wishart 1984, Martin et al. 1996, Aune et al. 1998, George et al. 2008).

Attempts to quantitatively test whether contact with domestic sheep poses a risk of die-off or extirpation of bighorn sheep populations have examined the correlation between population performance and distance from domestic sheep. Monello et al. (2001) analyzed population records of 99 bighorn sheep herds in western North America in an investigation of the ecological correlates of pneumonia epizootics. They found that bighorn sheep populations that had suffered a pneumonia-induced die-off were located, on average, significantly closer to domestic sheep allotments (24.1 ± 11.5 km) than either those that had not suffered a die-off or those that had suffered a die-off not induced by pneumonia (39.6 ± 8.5 km).

Singer et al. (2000) analyzed factors contributing to the success of 100 translocations of bighorn sheep and found that the 30 unsuccessful translocations were on average significantly closer to domestic sheep (6 ± km) than either modestly successful or successful translocations. Finally, based on an analysis of 24 herds, Singer et al. (2001) found that the persistence of bighorn sheep populations was significantly correlated with the presence of domestic sheep: populations located closer to domestic sheep were smaller and had lower population growth rates than bighorn populations located farther from domestic sheep.

Although these analyses indicate that bighorn sheep populations perform more poorly when they are closer to domestic sheep, they typically don’t include observations of contact, let alone the transmission of a pathogen from domestic sheep to bighorn sheep.

Evidence for Disease Transmission from Domestic Goats

The scientific literature regarding the potential for disease transmission from domestic goats to bighorn sheep is much less developed than that for domestic sheep. However, the literature shows that domestic goats and pack goats are physiologically capable of carrying the bacteria that are believed to be important in wild sheep die-offs, including *Pasteurellaceae* (*Pasteurella multocida*, *Mannheimia haemolytica,* and *Bibersteinia trehalosi*), and *Mycoplasma ovipneumoniae*.

Miller et al. (2011) compared the infectious agents present in multiple populations of bighorn sheep near to, and distant from, their interface with domestic sheep and domestic goats. One domestic goat population co-managed with a domestic sheep herd was included in this study. Domestic goats had 37 different *Pasteurellaceae* species or biovariants isolated. Half (50%) of domestic goat isolates were *P. (B.) trehalosi* (n = 102), and 44% were *M. haemolytica* (n = 89). The authors concluded that the diversity of *Pasteurellaceae* found in this study presented challenges for interpreting the results. They highlighted the uncertainties involved, and stated that more data was needed regarding the virulence of the different strains, whether they are primary or secondary causal agents, or whether they predispose animals to disease from other agents.

In a recent Washington state survey of goat farms adjacent to bighorn sheep habitat, *Mycoplasma ovipneumoniae* was carried asymptomatically by domestic goats on 7 of 16 farms, by 28% of all goats tested, and by 58% of individual goats on positive farms (Heinse et al. 2016).

Pack goats users have stated that their goats are maintained as small herds with little or no contact with other domestic sheep or goats, and thus have reduced potential to contract pathogens that could then be transmitted to bighorn sheep compared to either domestic sheep or other domestic goats. The results of Heinse et al. (2016) provide support for this assertion. These authors found that small flocks of domestic goats were more likely to test negative for *M. ovipneumoniae* (average = 4.1 for *M. ovipneumoniae* negative herds) compared to larger flocks of domestic goats (average = 30.3 for *M. ovipneumoniae* positive herds). They also noted that pure-breed flocks of domestic goats had a lower incidence of *M. ovipneumoniae* than mixed-breed flocks, and suggested that this was related to flock management practices and reduced frequency of contact with other flocks for pure-breed domestic goat flocks.

Ward et al. (2002) tested 45 pack goats from 9 different herds for the presence of *Pasteurellaceae* bacteria. *Pastuerella trehalosi* was isolated from all 45 goats, *Pastuerella haemolytica* was isolated from 38 goats, and *Pastuerella multocida* was isolated from 1 goat. The authors concluded that the strains of *Pastuerella haemolytica* isolated from pack goats in this study had not been previously associated with disease in bighorn sheep. However, strains of *Pastuerella trehalosi* isolated from 5 of the 9 pack goat herds tested had previously been identified as the cause of disease in bighorn sheep. The authors concluded that concern for transmission of disease-causing strains of *Pastuerella* spp. from pack goats to bighorn sheep was warranted.

Additionally, recent sampling of 575 domestic goats (421 of which were pack goats) conducted by Dr. Margaret Highland (USDA Agricultural Research Service, personal communication, 8/17/2017) showed a low prevalence of *M. ovipneumoniae* in pack goats, with 38 of 575 goats testing positive for this pathogen. Samples were taken in triplicate, with

a minimum of four weeks between sampling. Of the 38 test positive goats, 24 were less than one year old. Some of these goats tested positive once, and tested negative during subsequent tests. Goats testing positive just once were mostly attributed to having exposure to outside pack goat herds. In contrast to Heinse et al.'s (2016) results, in this study the number of pack goats on a premises was not strongly correlated with test results. The goats tested in this study were from 81 different premises in 13 states, 76 of which had no goats test positive for *M. ovipneumoniae* during repeat sampling, and several of which had goats test positive just once.

Experiments

There is experimental evidence indicating that domestic goats pose a disease transmission risk to bighorn sheep, but that the risk is less than that posed by domestic sheep. Three comingling studies have indicated domestic goats were less likely to transmit disease, and if disease transmission did occur it was often less virulent. However, the sample sizes involved in these three studies were low, and there is still uncertainty over the role of domestic goats in regards to bighorn sheep pneumonia. No experimental studies have been conducted specific to disease transmission from pack goats to bighorn sheep.

Foreyt (1994) comingled two bighorn sheep with three domestic goats purchased from a livestock auction yard for 60 days. At the end of the trial, both bighorn sheep remained healthy. In a subsequent study, Foreyt et al. (2009) comingled seven bighorn sheep with four domestic goats that were shedding lungworm larvae, with the result that two of the bighorn sheep died of bacterial pneumonia.

Besser et al. (2017) comingled *M. ovipneumoniae* test-negative domestic goats with healthy bighorn sheep for 100 days, after which comingled bighorn sheep showed no signs of respiratory disease. In the same study, healthy bighorn sheep comingled with *M. ovipneumoniae* test-positive domestic goats developed pneumonia, although the severity of the disease was notably milder than that reported in previous experiments conducted with domestic sheep-origin strains of *M. ovipneumoniae* (Besser et al. 2017). Both domestic goats and bighorn sheep in this study carried leukotoxic positive *Pasteurellacae* bacteria which have been thought to play a key role in bighorn sheep pneumonia, yet the presence of these bacteria was not clearly linked to development of pathologic lesions or experimental outcomes (Besser et al. 2017). However, this article also identified important questions regarding disease transmission between domestic goats and bighorn sheep that current research has not resolved, including whether domestic goats may carry more virulent strains of *M. ovi*, whether bighorn sheep that recover from infection of domestic goat strain *M. ovi* can become persistent carriers and transmit *M. ovi* to their lambs, and if that occurs whether lamb pneumonia could be induced (Besser et al. 2017).

Field Evidence of Large-scale, Rapid, All-age Die-offs

There is comparatively little literature demonstrating disease transmission from domestic goats to bighorn sheep in the field, and there have been no documented cases of pack goats transmitting disease to bighorn sheep. It is often difficult to definitively establish the causes of a bighorn sheep die-off in the field. Garde et al. (2005) recognized this, stating that, "there is rarely irrefutable evidence since most investigations occur following a disease event. Complicating this further has been the poor historical or sometimes ambiguous identification of the pathogens and often limited knowledge of their transmission dynamics."

The literature that does exist indicates that the probability of disease transmission following contact between domestic goats and bighorn sheep and the resulting severity are variable. For example, *Pasteurella* spp. were isolated from feral goats and bighorn sheep in the Hells Canyon National Recreation Area. The authors concluded that although the direction of transmission could not be established, evidence suggested transmission of strains from goats to bighorn sheep (Rudolph et al. 2003). However, there was no evidence that those organisms were responsible for subsequent bighorn sheep disease or mortality (Rudolph 2003). Although the timing of the sampling for this study coincided with an all-age bighorn sheep die-off from pneumonia, the ultimate causes of the disease outbreak remain unclear (Cassirer et al. 1996) and there is scientific debate concerning the validity of the Rudolph (2003) study (Dr. Margaret Highland, USDA-ARS, NAPGA comment on SEIS exhibit 2).

In addition to the Hells Canyon die-off discussed above, Coggins et al. (2002) reported on two additional bighorn sheep die-offs in Idaho and California where there was circumstantial evidence that domestic goats may have been the cause. These authors also concluded that there was evidence for domestic goats causing pneumonia outbreaks in bighorn sheep but that the evidence was not as strong as that for domestic sheep.

Drew et al. (2014) reported on three bighorn sheep that had known contact with domestic goats on grazing allotments or private property, along with another bighorn sheep that had contact with a mixed flock of domestic sheep and goats. Three of the bighorn sheep were periodically tested for *Pasteurellaceae* bacteria, and then euthanized and necropsied, and the fourth bighorn sheep had been killed in the field near where the contact with domestic goats had occurred. None of the four bighorn sheep had evidence of pneumonia, but various species and strains of potentially pathogenic bacteria were isolated from all four animals.

Cassirer et al. (2016) found that introduction of a new genotype (strain) of *M. ovipneumoniae* into a chronically infected bighorn sheep population in the Hells Canyon region of Washington and Oregon was accompanied by adult morbidity (100%) and pneumonia-induced mortality (33%) similar to that reported in epizootics following exposure of naïve bighorn sheep. Phylogenetic analysis showed that the strain associated with the outbreak was likely of domestic goat origin.

Sells et al. (2015) modelled the risk of pneumonia outbreaks using data from 43 bighorn sheep herds across Montana that experienced 22 die-offs from 1973-2013, in relation to a suite of variables. The variables that best predicted pneumonia outbreaks within a defined herd high risk area included the amount of private lands, whether domestic sheep and goats had been used for weed control, whether there was a history of disease outbreaks, and herd density within the high risk area. While this study indicated a strong relationship between risk of contact between bighorn sheep and domestic sheep and goats used for weed control in the development of pneumonia, an important limitation is that it did not specifically discriminate between domestic sheep and domestic goats in the analysis. Therefore, it is difficult to make inferences specific to domestic goats from this study.

Domestic goats can also carry other disease organisms with serious consequences for bighorn sheep (Jansen et al. 2006). In late 2003 and 2004, the Silver Bell bighorn herd in Arizona was infected with keratoconjunctivitis (KCS) caused by *Mycoplasma conjunctivae*. This is a highly contagious eye infection common in domestic sheep and goats (Whithear 2001). This disease is thought to spread via insect vectors or direct contact (Whithear 2001). Infection is characterized by redness of the eyes, blinking, and ocular discharge (Janovsky et al. 2001), but in some cases can lead to blindness (Giacometti et al. 2002). As a result of genetic

investigation, the source of the Silver Bell infection was believed to be direct contact with 4,800 domestic goats released into bighorn habitat (Jansen et al. 2006). Contagious ecthyma was also reported from the Silver Bell bighorn sheep herd incident. The outbreak of keratoconjunctivitis was followed by a large-scale and severe contagious ecthyma outbreak (Jansen et al. 2006). Contagious ecthyma, commonly called sore mouth, is endemic in domestic herds of sheep, goats, and llamas in western Canada (Garde et al. 2005). Lesions are typically restricted to the lips and muzzle on domestics while they can cover the entire body of bighorn sheep (Garde et al. 2005, Merwin and Brundage 2000). The condition can be very painful, interfering with chewing of food (Samuel et al. 1975), and resulting in loss of body condition (Garde et al. 2005). Although serious diseases, keratoconjunctivitis and contagious ecthyma do not have the same population level implications as bacterial pneumonia (Clark et al. 1993, L'Heureux et al. 1996). .

Long-term Implications of Die-offs

In contrast to most other wild and domesticated mammal species, bighorn sheep are notable in their extreme susceptibility to some strains of *Pasteurella* spp. (Miller 1991). In some cases, bighorn sheep disease events can have major population-limiting effects with die-offs affecting animals of all age classes, and resulting in prolonged periods of low lamb survival (Coggins 1988; Foreyt 1990; Coggins and Matthews 1992; Cassirer and Sinclair 2007; George et al. 2008; Besser et al. 2012a, b; Cassirer et al. 2013). It is hypothesized that once *Pasteurella* spp. have been introduced to bighorn sheep populations, they may become endemic and continue cycling for decades (Miller et al. 1991). The disease persists following mortality events and reduces reproductive success, preventing regrowth of the population (George et al. 2008).

When bighorn sheep experience a pneumonia episode, all-age mortality normally occurs. Low lamb survival rates typically continue after the initial die-off, delaying population recovery for years to decades (Foreyt 1990, Coggins and Matthews 1992, Ward et al. 1992, Foreyt 1995, Schommer and Woolever 2001, George et al. 2008; Cassirer et al. 2013, Manlove et al. 2016). Research indicates that lambs born in bighorn sheep herds that experienced a pneumonia episode typically die before 3 months of age (Foreyt 1990, Herndon et al. 2011, Wood et al. 2017). It is likely that surviving ewes remain carriers of pathogens for several years and transfer the bacteria to their lambs (Herndon et al. 2011, Wood et al. 2017). Lambs are protected by passive colostrum immunity early in life, but when this immunity wanes at 6 to 8 weeks of age, they may die from pneumonia.

Full population recovery following a die-off may require decades. Loss of genetic diversity and herd memory of historical migration routes may be irreplaceable.

Vaccines

Experimental trials to develop and test vaccines have been conducted, but are far from conclusive. In a pen experiment, four bighorn sheep repeatedly immunized with multivalent *Mannheimia-Bibersteinia* vaccine were protected from induced *Mannheimia haemolytica* pneumonia, while four non-vaccinated control bighorn sheep died within 48 hours of being infected (Subramaniam et al. 2011). However, strain-specific immunity could complicate efforts to develop vaccines (Cassirer et al. 2016). So far no vaccine has completely protected wild sheep commingled with domestic sheep in captive settings or shown potential for efficacy in free-ranging animals (Callan et al. 1991, Kraabel et al. 1998, Cassirer et al. 2001,

Subramaniam et al. 2011, Sirochman et al. 2012). A recent synthesis paper of bighorn sheep pneumonia and management options recognized that vaccines have been not been successful for mitigating respiratory disease in bighorn sheep (Cassirer et al. 2017). If successfully developed, vaccinations would be logistically difficult and expensive to administer (Wehausen et al. 2011); therefore, repeated vaccination in the wild may not be practical. Some investigators have offered that vaccination could play a role in developing and maintaining *M. ovipneumoniae*-free herds of domestic sheep or goats that could significantly reduce disease transmission risk to bighorn sheep (Cassirer et al. 2016, Cassirer et al. 2017), but such programs have not yet been developed.

Domestic Sheep Grazing on the Shoshone National Forest

Domestic sheep grazing on the SNF reached its highest point in the early 1900s and has been on a steady decline since. The initial decline was primarily due to stocking rate adjustments to achieve a more sustainable use of the rangeland. From the 1960s to 1980s, many sheep allotments were converted to cattle. Since then, all commercial sheep grazing permits on the SNF, except for one, have been removed.

Two active allotments (Table 1) on the southern end of the SNF comprise the current extent of domestic sheep grazing on the SNF. The permits for these two allotments were issued to the same permittee. Up to 1,150 ewe/lambs are grazed on the Pine-Willow Allotment, and are then moved to the adjacent Slate Creek Allotment. The Pine-Willow Allotment has two pastures identified, with grazing only permitted for the southern-most pasture. No domestic sheep grazing is authorized within core native bighorn sheep range on the SNF.

Table 1. Domestic sheep grazing allotments on the Shoshone National Forest

Allotment	Stocking Rate	Grazing Dates	Allotment Status
Pine-Willow	1,150 ewe/lamb	7/20 – 8/15	Active
Slate Creek[1]	1,150 ewe/lamb	8/16 – 9/10	Active

Pack Goat Use on the Shoshone National Forest

There are no active commercial domestic goat allotments on the SNF, and domestic goats are not used for vegetation management, but recreational goat packing is allowed on the Washakie Ranger District. The Forest Service does not track pack goat use, but information provided by pack goat users indicates that the Popo Agie Wilderness has been used by goat packers for years. Pack goat use levels in this area can be generally characterized as low.

On November 14, 2011, a temporary area closure order was signed and implemented restricting domestic goat use on the Clarks Fork, Wapiti, Greybull, and Wind River Ranger Districts. This closure was implemented to reduce the risk of disease transmission from pack goats to core native bighorn sheep herds (USDA Forest Service 2012*a*). The pack goat closure order was issued again in June 2016 and will be in effect until December 31, 2019, or until rescinded (Appendix A). Under this temporary closure, domestic goat use is only authorized on the Washakie Ranger District.

Pack goat use for back country trips into the Wind River Range occurred prior to implementation of the closure order. The primary destinations for goat packing have been in the Fitzpatrick Wilderness on the Wind River and Washakie Ranger Districts. Pack goat use

levels in this area can also be generally characterized as low, although the Forest Service has no data on use levels.

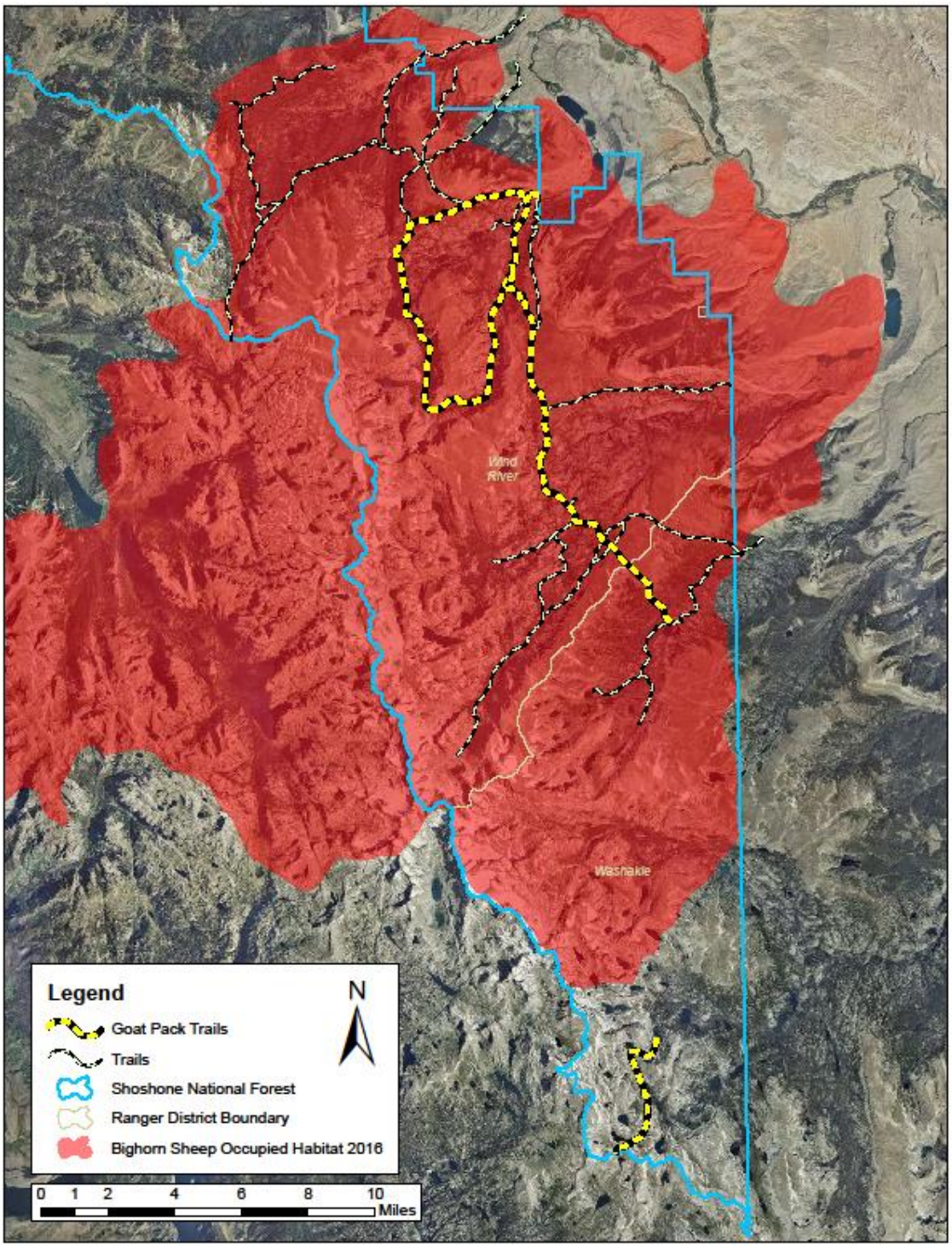

Figure 1. Trails used for goat packing prior to the 2011 and 2016 closure orders within the Whiskey Mountain bighorn sheep herd's occupied habitat on the Wind River and Washakie Ranger Districts.

Bighorn Sheep Status on the Shoshone National Forest

The SNF has the largest number of bighorn sheep of any forest within the National Forest System, with about 4,500 of the estimated 6,000 bighorn sheep in Wyoming (Table 2). Six of the eight core native bighorn sheep herds in Wyoming reside on the SNF. These core native herds include: Clarks Fork, Trout Peak, Wapiti Ridge, Younts Peak, Francs Peak, and Whiskey Mountain, which currently occupy 67% (1.65 million acres) of the SNF (Figure 2).

Table 2. Population estimates and demographic characteristics of six bighorn sheep populations on the Shoshone National Forest

[Source: WGFD 2017 a, b; –, no data]

Herd	Population Estimate	Population Objective	Lambs per 100 Ewes	2011–2015 Average	Rams per 100 Ewes	2011–2015 Average
Clarks Fork	600	500	21	31	43	31
Trout Peak	680	750	25	28	24	34
Wapiti Ridge	850	1000	31	23	27	28
Younts Peak	875	900	27	25	39	442
Francs Peak	710	1350	20	23	50	56
Whiskey Mountain	841	1350	18	30	47	49
Temple Peak[1]	–	–	–	–	–	–

[1] Comparable population data are not currently available for this cooperative review herd.

Five of the six core native herds on the SNF are connected to one another, (the Whiskey Mountain herd being the exception), and together form the Absaroka metapopulation. Natural interchange between these adjacent herds is thought to be greater than 10%. If interchange falls below 10%, WGFD considers the relevant herd units to be isolated from one another and functioning as discrete biological herds rather than as a metapopulation.

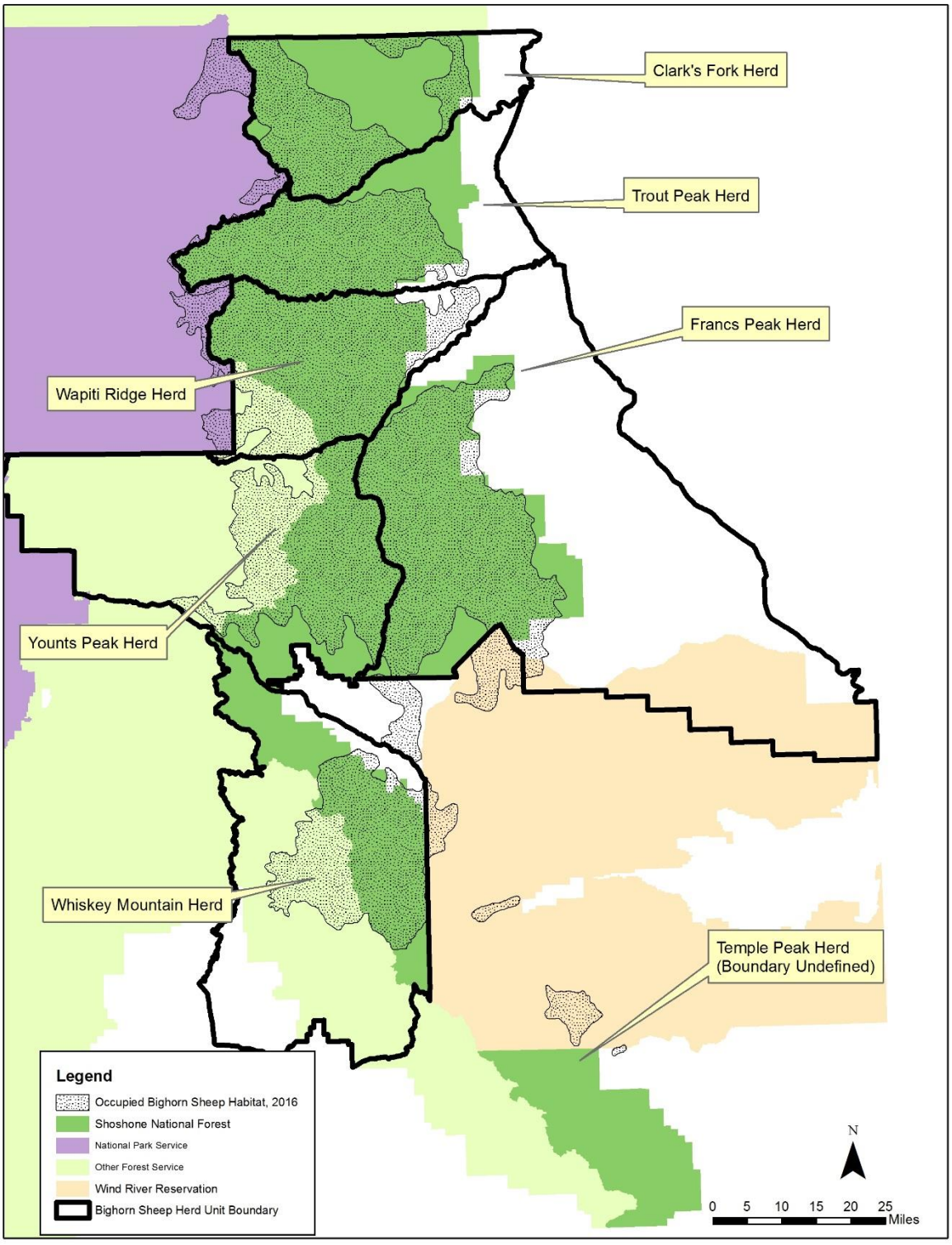

Figure 2. Bighorn sheep herds and occupied habitat on the Shoshone National Forest. The Clark's Fork, Trout Peak, Wapiti Ridge, Yount's Peak, and Francs Peak Herds collectively comprise the Absaroka Metapopulation.

Clarks Fork Bighorn Sheep Herd

This core native herd occupies mostly SNF lands in the Absaroka Range and Beartooth Plateau, with smaller portions found on adjacent portions of Yellowstone National Park and the Custer Gallatin National Forest. Population data for this herd is provided in Table 2. In recent years, this herd has been at or above management objectives, with good recruitment (WGFD 2017*a*).

No domestic sheep grazing occurs within this herd unit. The closest domestic sheep/goat grazing on the SNF is about 240 km (150 miles) south of the Clarks Fork herd (Table 3). No pack goat use is known to occur within this core native herd range.

Table 3. Proximity of bighorn sheep herds on the Shoshone National Forest to closest domestic sheep herd by land ownership and herd status

[km, kilometer; BLM, Bureau of Land Management; >, greater than]

Bighorn Sheep Herd	Proximity to Domestic Sheep on Shoshone National Forest (km)	Proximity to Domestic Sheep on adjacent lands (km)	Land Ownership of Adjacent Lands	Herd Status
Clarks Fork	240	2	Private	Core native herd
Trout Peak	221	19	BLM	Core native herd
Wapiti Ridge	179	29	BLM	Core native herd
Younts Peak	137	42	BLM	Core native herd
Francs Peak	113	33	BLM, Private	Core native herd
Whiskey Mountain	81	>60	Bridger-Teton National Forest	Core native herd
Temple Peak	29	Unknown	Unknown	Cooperative review herd

Trout Peak Bighorn Sheep Herd

This core native herd occupies portions of the SNF within the Absaroka Range, with a small number also utilizing adjacent portions of Yellowstone National Park. Population data for this herd is provided in Table 2.This herd has been at or slightly below management objectives in recent years (WGFD 2017*a*). No domestic sheep grazing occurs within this herd unit. The closest domestic sheep/goat grazing on the SNF is about 221 km (138 miles) south of the Trout Peak herd. No pack goat use is known to occur within this core native herd range.

Wapiti Ridge Bighorn Sheep Herd

This core native herd occupies portions of the SNF and BTNFs within the Absaroka Range, with a small number also utilizing adjacent portions of Yellowstone National Park. Population data for this herd is provided in Table 2. The population appears to be exhibiting a downward trend in recent years, and is currently below management objectives (WGFD 2017*a*). No domestic sheep grazing occurs within this herd unit. Closest domestic sheep/goat

grazing on the SNF is about 179 km (112 miles) south of the Wapiti Ridge herd. No pack goat use is known to occur within this core native herd range.

Younts Peak Bighorn Sheep Herd

This core native herd occupies portions of the SNF and BTNF within the Absaroka Range. Younts Peak is the most remote bighorn sheep herd in Wyoming **(**Beecham et al. 2007**)**. While much of the Younts Peak herd is non-migratory and resides year-round on high-elevation ridges (Wyoming Game & Fish Department 2017a), portions of this herd do move to low-elevation winter range in the South Fork of the Shoshone River valley. The large number of sheep wintering at high elevations make this herd prone to periodic high mortality losses from severe winter weather.

Population data for this herd is provided in Table 2. The population is recovering from high winter mortality during 2010-2013, and is currently near management objectives (WGFD 2017*a*). No domestic sheep grazing occurs within this herd unit. The closest domestic sheep/goat grazing on the SNF is about 137 km (85 miles) southeast of the Younts Peak herd. No pack goat use is known to occur within this core native herd range.

Francs Peak Bighorn Sheep Herd

This core native herd occupies portions of the SNF and the Wind River Indian Reservation within the Absaroka and Owl Creek Ranges. Population data for this herd is provided in Table 2. This herd declined by 40-50% after the winter of 2010-2011 due to mortality associated with winter weather and a possible disease outbreak. The population is now believed to have stabilized or increased slightly but is still well below management objectives (WGFD 2017*a*).

The closest domestic sheep/goat grazing on the SNF is about 113 km (70 miles) south of the Francs Peak herd. No pack goat use is known to occur within this core native herd range.

Whiskey Mountain Bighorn Sheep Herd

This core native herd occupies portions of the SNF and BTNF and the Wind River Indian Reservation within the Wind River Range (Figure 2). Population data for this herd is provided in Table 2. This was once the largest herd in the country, but after a catastrophic all-age die-off from pneumonia in 1991, the population has yet to recover and has been below objective for the past 20 years (WGFD 2017b).

In 2010, WGFD personnel spent a significant amount of time observing sheep in early fall as they arrived on winter range. Many lambs were observed coughing violently and showing symptoms of pneumonia. Eleven sheep were euthanized throughout the fall and examined at the Wyoming state veterinary lab to document the presence of disease. Examinations revealed *Mycoplasma ovipneumoniae* in all the sheep that had been seen coughing violently. It appears likely that persistent, low annual recruitment in this population can be traced to chronic bacterial infection resulting in significant lamb mortality as sheep migrate onto winter range in the fall. Despite low recruitment, the population is growing very slowly and it

appears a small increase in lamb recruitment will stabilize this population. However, persistent chronic pneumonia continues to be a problem in this herd (Anderson, WGFD, pers. comm. 2017).

The Whiskey Mountain herd is isolated from other herds on the SNF. The Highway 26 corridor, which is the dividing line between the Whiskey Mountain herd and core native herds to the north, consists of fairly unsuitable bighorn sheep habitat, which limits interchange with the Absaroka metapopulation (Beecham et al. 2007). Furthermore, connectivity between the Whiskey Mountain and Temple Peak herds has not been demonstrated (McWhirter, WGFD, pers. comm. 2017).

No domestic sheep grazing occurs within this herd unit. The closest domestic sheep grazing on the SNF is about 81 km southeast of the Whiskey Mountain herd (Table 3).

Pack goat use is currently prohibited within most of this herd's range. However, as currently written, the closure order still allows pack goat use in the Fitzpatrick Wilderness on the Washakie Ranger District, which encompasses the southern portion of the Whiskey Mountain herd's home range (Appendix A).

In the past, pack goat use occurred on the SNF within the occupied habitat of this core native herd (Figure 1). Specific trails (about 38 miles) used by goat packing enthusiasts in the Fitzpatrick Wilderness in the past have been identified (North American Packgoat Association 2011). About 33 miles of the trails identified are within currently occupied bighorn sheep habitat within the Whiskey Mountain herd range (Figure 1). The only pack goat outfitter to operate in this area on the SNF relinquished their permit in 2007.

Temple Peak Bighorn Sheep Herd

The Temple Peak herd is comprised of a remnant herd along with descendants of 188 bighorn sheep transplanted from the nearby Whiskey Mountain Herd from 1960-1987, and an additional 88 transplanted to the Wind River Indian Reservation in 1988 and 1993. These sheep primarily used habitat in Sinks Canyon, North Fork Popo Agie Canyon, Little Popo Agie Canyon, and the South Fork of the Little Wind River. This herd experienced an all-age pneumonia die-off in 1992 and has never recovered (WGFD 2007), although it appears to have increased slightly in recent years. Based on recent observations and GPS collar data from bighorn sheep captured in 2016 and 2017, the current distribution of bighorns includes a small number in the North Fork of the Popo Agie River (Stan Harter, Wyoming Game & Fish Department, personal communication, 8/25/2017), with additional animals from the Wind River Indian Reservation migrating to high elevation summer range in the South Fork of the Little Wind River and Cirque of the Towers (Wyoming Game & Fish Department, unpublished data). Some collared bighorn sheep also remained year-round on the Wind River Indian Reservation. No movement has been document south of the North Fork of the Popo Agie River drainage in recent years. Additionally, connectivity between the Temple Peak and Whiskey Mountain herds has not been established, although recent GPS collar data from bighorn sheep in the Bull Lake Creek drainage indicate this is a possibility.

A home range for this herd has not been defined due to the lack of data. This herd no longer has a hunt area assigned to it and is not discussed in the WGFD Annual Big Game Herd Unit Reports. The Temple Peak herd is not a core native herd; rather, it is a transplanted herd and is designated a "Cooperative Review Area" by the State of Wyoming (Wyoming State-wide

Bighorn/Domestic Sheep Interaction Working Group 2004). Cooperative Review Areas contain suitable bighorn sheep range where proposed changes in bighorn sheep management or domestic sheep use will be cooperatively evaluated.

Including animals on the Wind River Indian Reservation, the Temple Peak herd currently consists of about 100 sheep (McWhirter, WGFD, pers. comm. 2017). Cassaigne et al. (2010) suggest that a minimum population of 188 bighorn sheep is required to ensure long-term persistence in the presence of epizootic disease. Therefore, this herd may eventually go extinct. The WGFD is not currently considering supplementations into this herd (McWhirter, WGFD, pers. comm. 2017).

Domestic sheep grazing has occurred on both the SNF and BTNFs within this herd's historic summer range, but not within currently occupied range. GPS collar data from 2016-2017 show that the closest bighorn sheep occupied habitat is approximately 27 km (17 miles) from the active domestic sheep grazing allotments on the SNF (Stan Harter, Wyoming Game & Fish Department, personal communication, 8/25/2017). Suitable bighorn sheep habitat within the domestic sheep allotments on the SNF is very limited due to its forested nature. In addition, a large portion of the land between the allotments and the Temple Peak herd's current occupied habitat is forested, which inhibits bighorn sheep forays to these allotments. Pack goat use occurs within the occupied habitat of this cooperative review herd.

Disease Status of Bighorn Sheep Herds on the Shoshone National Forest

The Wyoming Game & Fish Department conducted capture operations for all bighorn sheep herds on the Shoshone National Forest for disease surveillance and other purposes from 2011-2017. The results indicate that all the herds harbor a broad array of pathogens that have been identified in the literature as being important factors in bighorn sheep pneumonia outbreaks. For bighorn sheep from the Absaroka metapopulation and Whiskey Mountain herds, leukotoxin positive *Bibersteinia trehalosi, Mannheimia haemolytica*, and *Mannheimia spp* (various species of *Mannheimia* that are thought to be uncommon causes of respiratory disease), *Mycoplasma ovipneumoniae,* and *Pasteurella multocida* were all detected. Bighorn sheep from the Temple Peak herd had similar results, except that leukotoxin positive *Bibersteinia trehalosi* was not detected (Hank Edwards, Wyoming Game & Fish Department, personal communication, 08/23/2017).

The results of this disease surveillance work do not diminish the concern for disease transmission from domestic sheep, domestic goats, or pack goats to bighorn sheep on the Shoshone National Forest. It is possible that in some cases the strains currently carried by bighorn sheep in these herds may be less virulent, or that these bighorn sheep have developed some level of immunity specific to those strains. Contact between domestic sheep or goats and bighorn sheep has the potential for transmission of novel agents to naïve bighorns (Miller et al. 2011). Casirrer et al. (2016) provided evidence for introduction of a novel *Mycoplasma ovipneumoniae* strain to bighorn sheep from domestic goats in the Hells Canyon area that led to a pneumonia outbreak, and explained that immunity from past exposure may be strain-specific. In fact, this study documented that bighorn sheep with higher antibody titers for *Mycoplasma ovipneumoniae* prior to exposure to the new strain had lower survival rates after exposure, suggesting a harmful autoimmune response.

Methods

As stated earlier, an August 2011 letter from the Deputy Chief of the Forest Service outlined an approach to risk assessment and viability analysis (USDA Forest Service 2011). The analysis process outlined in the letter consists of four steps:

1. Gather applicable data and information from appropriate sources.
2. Assess spatial and temporal overlap of bighorn sheep core herd home ranges with domestic livestock allotments, use areas, and driveways.
3. Assess likelihood of contact (low, moderate, high) based on spatial and temporal overlap between domestic livestock use areas and bighorn sheep herds.
4. Identify management practices with the goal of separation between domestic livestock and bighorn sheep where necessary to provide for Forest-wide bighorn sheep viability.

This RADT follows that four-step process. A subsequent letter (USDA Forest Service 2012b) expanded the approach to include domestic goat grazing, and we believe using this approach is generally applicable to evaluating risk from pack goats as well.

Qualitative risk assessment is a commonly used method to determine where risk exists and how it can be mitigated. In this RADT report, qualitative information is used to determine the risk of physical contact between bighorn sheep and domestic sheep or goats. This level of analysis is commensurate with the complexity of the management situation on the SNF. The only bighorn sheep herd on the SNF in proximity to domestic sheep allotments on the SNF is the Temple Peak herd. Because the data currently available for the Temple Peak herd are not sufficient to accurately delineate its core herd home range (USDA Forest Service 2017b), and because no other bighorn herd on the SNF is within 35 km of a domestic sheep allotment on the SNF, the Bighorn Sheep Risk of Contact Tool was not used for this analysis (USDA Forest Service 2013). Quantitatively modeling the risk of contact from domestic sheep on lands outside the jurisdiction of the SNF was beyond the scope of this analysis. The quantitative Risk of Contact Model was not appropriate to use for modelling risk of contact between pack goats and bighorn sheep because it was developed for application to domestic sheep grazing allotments, and because temporal and spatial overlap between the two is already known based on where pack goat use is reported to have occurred relative to occupied bighorn sheep habitat on the Forest. Additionally, due to the lack of available data and substantial uncertainty regarding the numerous factors associated with the probability of actual contact occurring between pack goats and bighorn sheep, and the potential risk of disease transmission between the two if contact were to occur, a quantitative method could not be used.

The scale of this risk assessment is the planning unit, in this case the SNF. The main focus is on active domestic sheep allotments and areas that have been identified as pack goat use areas within the SNF. Recognizing the limits of SNF regulatory authority, this assessment also considers the potential cumulative impacts from adjacent lands outside the boundary of the SNF.

Steps 1 and 2

Gather applicable data and assess spatial and temporal overlap between domestic livestock use areas and bighorn sheep herds

See the three previous sections of this RADT: *Domestic Sheep Grazing on the Shoshone National Forest*, *Domestic Goat Use on the Shoshone National Forest*, and *Bighorn Sheep Status on the Shoshone National Forest*.

Step 3

Assess likelihood of contact (low, moderate, high) based on spatial and temporal overlap between domestic livestock use areas and bighorn sheep herds

The sequence of events by which contact between bighorn sheep and domestic sheep or goats in a permitted grazing allotment or pack goat use area located outside a bighorn core home range might occur can be broken down into a number of steps. First, to reach a domestic sheep allotment or pack goat use area, a bighorn sheep must:

1. leave its core home range,
2. travel far enough to reach the domestic sheep grazing allotment or pack goat use area, and
3. intersect the allotment or pack goat use area.

For disease transmission to occur, the bighorn must:

4. come into physical proximity to a domestic sheep or goat in the allotment or pack goat use area, and
5. contract a disease from the domestic sheep or goat.

Finally, for a disease outbreak to affect the bighorn's home herd, the infected bighorn must:

6. return to their, or another herd's, core home range, and
7. transmit disease to other members of their, or another, herd.

For domestic sheep allotments or pack goat use areas that overlap portions of a bighorn core home range, steps 1–3 and 6 do not need to occur, thereby likely increasing the potential for a disease transmission event to occur, and also likely increasing the potential for a subsequent disease outbreak in the bighorn home herd.

Rationale for Risk Rankings

The risk of physical contact between bighorn sheep and a domestic sheep allotment or pack goat use area was given a qualitative rating of "High," "Moderate," or "Low" based on factors relating to spatial and temporal separation, along with other considerations such as the frequency of use, number of domestic sheep or goats involved in that use, and other factors related to human control over domestic sheep or goats. Risk of disease transmission with a subsequent bighorn mortality event, however, was not modeled quantitatively. Instead, a qualitative assessment of disease transmission risk was made considering the risk of contact

along with other factors such as disease prevalence, pathogen virulence, and potential for transmission.

- A rating of "High" risk indicates that contact between domestic sheep and goats and bighorn sheep is thought to be likely in the immediate future, although disease transmission resulting in a subsequent bighorn mortality event is not assumed to be a certainty. Conversely, if allotments have been operated for many years without evidence of disease transmission, we do not use this observation to infer a lower risk rating. The fact that contact has not been observed, or a bighorn disease event has not been detected, does not imply a lower risk for such events happening in the future. A rating of "High" risk would occur when there is direct overlap between an area of domestic livestock use and mapped bighorn range, or when these areas are within 10 miles (17 km) of an allotment there is good bighorn source habitat connectivity for bighorn dispersal.
- A rating of "Moderate" risk indicates that physical contact between bighorn and domestic sheep and goats may occur at some point in the future. Factors that reduce the apparent risk of contact could include the presence of towns, the presence of terrain features and/or habitat features that act as barriers to bighorn sheep movement (Schommer and Woolever 2001), and bighorn sheep distribution patterns. A rating of "Moderate" risk could occur when there is no direct overlap between mapped bighorn range, these areas are 10 to 21 miles (18 to 35 km) from an allotment, and/or there is fair bighorn source habitat connectivity for bighorn dispersal. It could also occur when there is direct overlap between a pack goat use area and mapped bighorn sheep range.
- A rating of "Low" risk indicates that physical contact between domestic sheep and goats and bighorn sheep is believed to be unlikely or irregular and unpredictable. A rating of "Low" risk could occur when there is no direct overlap between mapped bighorn range, and these areas are greater than 21 miles (35 km) from an area of domestic livestock use and/or there is poor bighorn source habitat connectivity for bighorn dispersal. It could also occur when there is direct overlap between mapped bighorn sheep range and pack goat use areas but mitigation measures are in place to limit the potential for contact, or when unmitigated pack goat use areas are 10-21 miles from mapped bighorn sheep habitat.

Assessment of Risk from Domestic Sheep and Goats and Pack Goats by Herd Unit

The Absaroka Metapopulation – Clarks Fork, Trout Peak, Wapiti Ridge, Younts Peak, and Francs Peak Herds

None of these core native bighorn sheep herds have occurred close (within 112 km) to domestic sheep allotments on the SNF in recent history (Table 3). All domestic sheep allotments within these herd units on the SNF have been closed or converted to cattle due to the willingness of grazing permittees to move to other allotments. Although the foray distances or probabilities for bighorn sheep on the SNF are not known, no occupied habitat for core native herds occurs within 35 km of domestic sheep allotments on the SNF. Because of the low risk of contact as a result of domestic sheep grazing activities on the SNF (Table

4), there is very little disease transmission risk from domestic sheep grazing on the SNF to these herds.

Table 4. Risk of contact ratings and herd status of bighorn sheep herds on the Shoshone National Forest

[Rationale for risk ratings is provided in text.]

Bighorn Sheep Herd	Risk rating from domestic sheep on SNF	Pack goat use in occupied bighorn sheep habitat allowed	Pack goat use in occupied core native bighorn sheep habitat prohibited	Herd status
Clarks Fork	Low	Moderate	Low	Core native
Trout Peak	Low	Moderate	Low	Core native
Wapiti Ridge	Low	Moderate	Low	Core native
Younts Peak	Low	Moderate	Low	Core native
Francs Peak	Low	Moderate	Low	Core native
Whiskey Mountain	Low	Moderate	Low	Core native
Temple Peak	Low	Moderate	Moderate	Cooperative review

Pack goat use is not currently known to have occurred within any of the Absaroka core native bighorn sheep ranges, and the area has generally been characterized by pack goat users as undesirable for pack goat use due to the high densities of large carnivores. However, the Forest Service has had a small number of inquiries in recent years from people potentially interested in using pack goats in these areas, including one request in 2016 from a person interested in using pack goats to support a bighorn sheep hunt. If there were no prohibition on pack goat use in these areas, it is reasonable to assume that pack goat use would occur on occasion, and this could include situations where there was spatial and temporal overlap between pack goats and bighorn sheep. This assumption was made because there is no data on specifically where pack goat use would occur in this area, and bighorn sheep in the Absaroka metapopulation occupy broad areas of the landscape (Figure 2).

Considering the evidence for social attraction between bighorn sheep and domestic goats as discussed elsewhere in this document, spatial and temporal overlap could lead to contact between bighorn sheep and pack goats. Contact could occur either through bighorn sheep approaching pack goats along the trail or in camps, or from lost pack goats approaching bighorn sheep. The risk of contact would be moderated by a number of factors including the low frequency of pack goat use expected, human presence typically associated with pack goat use, and the much greater ability of pack goat users to control their animals compared to free ranging domestic animals on a grazing allotment. Pack goat users have greater control over their animals due to the small number of animals generally involved and the high degree of bonding pack goats typically exhibit with their human associates. There would be a "moderate" risk of contact between bighorn and pack goats because contact may occur at some point in the future (Table 4).

If contact were to occur between pack goats and bighorn sheep, there would be relatively low potential for disease transmission resulting in impacts to bighorn sheep herds, but current

science suggests the potential for disease transmission between pack goats and bighorn sheep is lower than that expected from domestic sheep. This is based on literature reviewed earlier in this document demonstrating that domestic goats and pack goats can carry pathogens that have regularly been associated with pneumonia in bighorn sheep and the evidence presented for disease transmission from domestic goats to bighorn sheep. Literature reviewed earlier in this document discusses emerging science indicating that for several reasons domestic goats likely have lower disease transmission potential than domestic sheep, that this potential may be even lower for pack goats, and that pathogens transmitted from domestic goats have typically been less virulent than those transmitted by domestic sheep. However, it also describes the scientific uncertainty that still exists regarding disease dynamics among domestic goats, pack goats, and bighorn sheep.

Whiskey Mountain Herd

This core native bighorn sheep herd has not occurred close (within 81 km) to domestic sheep allotments on the SNF in recent history. In the past, domestic sheep from active domestic sheep allotments on the BTNF have wandered into occupied habitat of the Whiskey Mountain herd. However, those domestic sheep allotments on the BTNF have now been closed (USDA Forest Service 2017b). As a result, no known domestic sheep grazing occurs within 35 km of this herd, either on the SNF or BTNF (Table 3). Therefore, the risk of contact to this herd from domestic sheep grazing on National Forest lands is currently considered “low”, with very little disease transmission risk.

Goat packing has regularly occurred within the occupied habitat of this core native herd in the past (Figure 1), but has been prohibited by special order since 2011. A portion of the trails historically used for goat packing in the Fitzpatrick Wilderness are within and adjacent to areas consistently used by bighorn sheep, including rocky escape cover and open alpine meadows (Figure 3). These trails are in year-round bighorn sheep habitat. Without a prohibition on pack goat use there would be spatial and temporal overlap between pack goats and bighorn sheep. Considering the evidence for social attraction between bighorn sheep and domestic goats discussed elsewhere in this document, spatial and temporal overlap could lead to contact between bighorn sheep and pack goats. Contact could occur either through bighorn sheep approaching pack goats along the trail or in camps, or from lost pack goats approaching bighorn sheep. The risk of contact would be moderated by a number of factors including the low frequency of pack goat use expected, human presence typically associated with pack goat use, and the much greater ability of pack goat users to control their animals compared to free ranging domestic animals on a grazing allotment. Pack goat users have greater control over their animals due to the small number of animals generally involved and the high degree of bonding pack goats typically exhibit with their human associates. There would be a “moderate” risk of contact between bighorn and pack goats because contact may occur at some point in the future (Table 4).

If contact were to occur between pack goats and bighorn sheep, there would be relatively low potential for disease transmission resulting in impacts to bighorn sheep herds, but current science suggests the potential for disease transmission between pack goats and bighorn sheep is lower than that expected from domestic sheep. This is based on literature reviewed earlier in this document demonstrating that domestic goats and pack goats can carry pathogens that have regularly been associated with pneumonia in bighorn sheep and the evidence presented

for disease transmission from domestic goats to bighorn sheep. Literature reviewed earlier in this document discusses emerging science indicating that domestic goats likely have lower disease transmission potential than domestic sheep, that this potential may be even lower for pack goats, and that pathogens transmitted from domestic goats have typically been less virulent than those transmitted by domestic sheep. However, it also describes the scientific uncertainty that still exists regarding disease dynamics among domestic goats, pack goats, and bighorn sheep.

Temple Peak Herd

The closest portion of the Temple Peak herd is about 27 km from domestic sheep allotments on the SNF. These allotments provide very limited suitable bighorn sheep habitat because they are mostly forested. In addition, there is a high amount of unsuitable forested landscape between currently occupied habitat for these two herds and the allotments. Furthermore, in recent years bighorn sheep have not been observed south of the North Fork of the Popo Agie River drainage. Domestic sheep grazing in the Pine-Willow sheep allotment is only authorized on the pasture south of Rennecker Peak. This means that not all of the acreage in the two allotments is utilized for domestic sheep grazing, and the area where domestic sheep grazing is authorized is located furthest from where bighorn sheep could occur. All of these factors reduce the current likelihood of bighorn sheep making contact with sheep allotments on the SNF. Therefore the risk of contact from domestic sheep grazing on the SNF is currently “low” for this cooperative review bighorn sheep herd with a low level of disease transmission risk.

Goat packing occurs within occupied habitat of this cooperative review herd. Portions of trails used for goat packing are within and adjacent to habitat used by bighorn sheep. These trails are in year-long bighorn sheep habitat; therefore, there is spatial and temporal overlap between goat packing and bighorn sheep. This increases the opportunities for contact between bighorn sheep and pack goats. Considering the evidence for social attraction between bighorn sheep and domestic goats discussed elsewhere in this document, spatial and temporal overlap could lead to contact between bighorn sheep and pack goats. Contact could occur either through bighorn sheep approaching pack goats along the trail or in camps, or from lost pack goats approaching bighorn sheep. The risk of contact would be moderated by a number of factors including the low frequency of pack goat use expected, human presence typically associated with pack goat use, and the much greater ability of pack goat users to control their animals compared to free ranging domestic animals on a grazing allotment. Pack goat users have greater control over their animals due to the small number of animals generally involved and the high degree of bonding pack goats typically exhibit with their human associates. There would be a “moderate” risk of contact between bighorn and pack goats because contact may occur at some point in the future (Table 4).

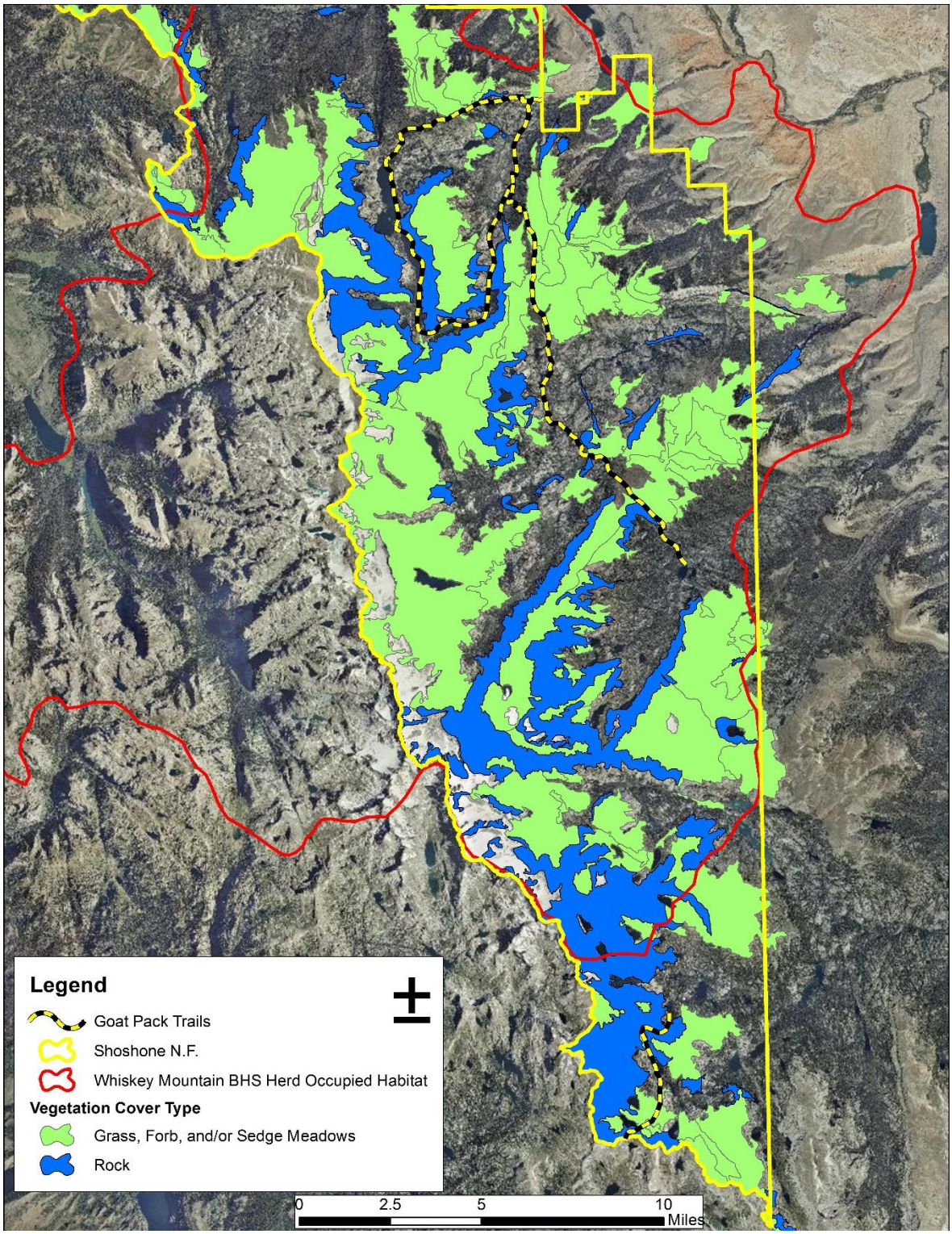

Figure 3. Potentially suitable bighorn sheep habitat and historically used goat packing trails within the Whiskey Mountain bighorn sheep herd's occupied habitat.

If contact were to occur between pack goats and bighorn sheep, there would be relatively low potential for disease transmission resulting in impacts to bighorn sheep herds, but current science suggests the potential for disease transmission between pack goats and bighorn sheep is lower than that expected from domestic sheep. This is based on literature reviewed earlier in this document demonstrating that domestic goats and pack goats can carry pathogens that have regularly been associated with pneumonia in bighorn sheep and the evidence presented for disease transmission from domestic goats to bighorn sheep. Literature reviewed earlier in this document discusses emerging science indicating that domestic goats likely have lower disease transmission potential than domestic sheep, that this potential may be even lower for pack goats, and that pathogens transmitted from domestic goats have typically been less virulent than those transmitted by domestic sheep. However, it also describes the scientific uncertainty that still exists regarding disease dynamics among domestic goats, pack goats, and bighorn sheep.

Step 4

Identify management practices with the goal of separation between domestic livestock and bighorn sheep where necessary to provide for Forest-wide bighorn sheep viability

Spatial and/or Temporal Separation

Separating domestic sheep allotments, domestic goats, and wild sheep habitat is widely recognized as the most viable current management option to prevent the spread of disease from domestic sheep and goats to wild sheep (Foreyt 1989, Cahn et al. 2011, WAFWA 2012, O'Brien et al. 2014, The Wildlife Society 2015). Most wildlife biologists and veterinarians have now concluded that bighorn and domestic sheep and goats should not occupy the same ranges or be managed in close proximity to each other (Foreyt and Jessup 1982, Goodson 1982, Coggins 1988, Onderka and Wishart 1988, Foreyt 1989, Foreyt 1990, Callan et al. 1991, Coggins and Matthews 1992, Foreyt 1992b, Foreyt et al. 1994, Foreyt 1995, Martin et al. 1996, WAFWA 2012, The Wildlife Society 2015). Consequently, current recommendations for minimizing pneumonia outbreaks in bighorn sheep are to maintain spatial or temporal separation between bighorn sheep and domestic sheep and goats on native ranges at all times (Schommer and Woolever 2001, WAFWA 2012, The Wildlife Society 2015). However, effective separation is complicated by the tendency of bighorn sheep, both rams and ewes, to leave their core herd home range and carry out occasional exploratory forays. Until recently, the primary management recommendation used for interspecies separation was the use of a standard buffer distance (e.g., 14.5 km) to reduce the potential for contact, but this is not applicable across all National Forest situations and bighorn sheep habitats. Singer et al. (2001) recommend focusing management for persistent bighorn sheep populations on large habitat patches more than 23 km from domestic sheep. However, Monello et al. (2001) analyzed population records of 99 bighorn sheep herds ranging from the southwestern United States to Alaska, in an investigation designed to discover the ecological correlates of pneumonia epizootics. They found that bighorn sheep populations that had suffered a pneumonia-induced die-off were located on average significantly closer to domestic sheep allotments (24.1 ± 11.5 km) than either those that had not suffered a die-off or those that had suffered a die-off not induced by pneumonia (39.6 ± 8.5 km). The minimum

buffer used in Hells Canyon was 25 miles (41 km) and yet was not effective in separating the species (Schommer and Woolever 2001).

Management recommendations specific to pack goat use in bighorn sheep habitat have also been suggested, but they are more variable compared to recommendations designed for domestic sheep and goat grazing situations. The most assertive expression of the need for separation was found in the WAFWA (2012) recommendations, which are that "the use of domestic sheep or goats as pack animals by persons who travel in identified wild sheep habitat should be prohibited by the appropriate management agency." Ward et al. (2002) suggested that pack goats should be managed to prevent contact with wild ruminants. Coggins (2002) cited a 1998 letter to goat packers by the State of Idaho recommending that they should avoid approaching wildlife less than 50 feet. The U.S. Animal Health Association Committees on Wildlife Disease and Sheep and Goats (USAHA 2009) recommended that pack goats should be tethered when not being trailed. More recently, Dr. Thomas Besser stated in a popular press article that "the expected low prevalence of carriage of *M. ovipneumoniae* by pack goats is currently being tested… if that low prevalence is confirmed, and unless new information rises to the contrary, I believe that *M. ovipneumoniae* test-negative pack goats represent a negligible risk for triggering pneumonia outbreaks in bighorn sheep and that it would be reasonable to take this into account when setting public lands policy (Besser 2016)." This statement seems to imply the author's position that *M. ovipneumoniae* is the key pathogen of concern in bighorn sheep pneumonia, and that spatial and temporal separation between pack goats and bighorn sheep may not be necessary if adequate disease-testing programs for this pathogen can be implemented for pack goats (as discussed later in this document).

If a prohibition on pack goat use were in place for the core native Absaroka metapopulation and Whiskey Mountain bighorn sheep herds, there would be effective spatial and temporal separation between domestic pack goats and bighorn sheep. As a result, there would be a "low" risk of contact between pack goats and bighorn sheep and essentially no disease transmission risk (Table 4), along with very low uncertainty regarding this risk.

Proposed Mitigation Measures for Pack Goats

During the Forest Plan revision process, a variety of mitigation measures were proposed by the North American Pack Goat Association to provide for separation between pack goats and bighorn sheep and reduce the risk of disease transmission (Jennings 2011). Some were considered to be infeasible and were not considered further. The mitigation measures determined to be feasible include:

1. Implementing a system that would require a permit for all pack goat use. Pack goat users would be informed on required and recommended actions for reducing the risk of contact between pack goats and bighorn sheep when obtaining their permit.
2. Requiring any observed contact between pack goats and bighorn sheep, as well as any lost pack goats, to be reported to the Forest Service as soon as possible as a condition of obtaining a pack goat use permit.
3. Limiting the number of pack goats per party.
4. Requiring pack goats be leashed or in direct control by their owners.

5. Requiring pack goats be high-lined or restrained in campsites.
6. Requiring pack goats to have bells attached to their collars at all times.
7. Requiring veterinary health inspection and disease testing of all pack goats before entering Shoshone National Forest lands, and requiring handlers to be in possession of a health and disease testing certificate for each pack goat.

Mitigation measure 1 would ensure that pack goat users understood the required and recommended actions for preventing contact between their pack goats and bighorn sheep. It would also help to track pack goat use on the Forest, and provide a mechanism to require reporting of any contact between pack goats and bighorn sheep. Reporting of lost pack goats could facilitate recovery efforts before contact with bighorn sheep occurred, and would help track how often this occurred. However, pack goat users may be disinclined to report contact between their goats and bighorn sheep, or even lost goats, for fear of incurring additional restrictions on their use. Implementation of mitigation measures 3, 4, and 5 would further increase the amount of control users would have over their pack goats and would help reduce the risk of contact between pack goats and bighorn sheep. Limiting the number of pack goats would allow greater control because fewer animals are easier to control. Requiring goats to be leashed together while traveling down the trail and high-lined in campsites would improve control of pack goats and reduce the risk of contact with bighorn sheep. Pack goats readily bond to their human handlers and have a strong desire to stay with them (Jennings 2011). The use of bells would allow users to track the movements of their goats.

However, users may not always be able to control their pack goats despite implementation of these techniques. Pack goat use occurs in remote, rugged settings where circumstances cannot always be controlled, and pack goats occasionally are lost on the Forest for a variety of reasons such as being scattered by predators or having too many tied on a high-line. Experienced goat packers have recognized that pack goats occasionally become lost, and that even conscientious pack goat users may not always be successful controlling their goats (J. Dirks, email conversation with J. Harper, Forest Service Wildlife Biologist, 2011). Additionally, it is perceived as dangerous to have goats tied together by leads when travelling through difficult terrain, and users typically disconnect them from each other in such settings (Jennings 2011). Uncontrolled or lost goats within bighorn sheep habitat could have direct contact with bighorn sheep.

In addition, the movements of bighorn sheep cannot be controlled. Wild sheep are unpredictable in their movements and could potentially come into contact with pack goats as well as other wild sheep. As discussed earlier in this analysis, bighorn sheep and domestic sheep and goats are socially attracted to each other, which increases the probability that they will make the close contact necessary for disease transmission. This could occur even under a scenario where pack goats were under close control as required by mitigations 4 and 5.

The mitigation measures are expected to reduce the risk of contact somewhat between pack goats and bighorn sheep, and contact between pack goats and bighorn under this scenario is expected to be irregular and unpredictable. Using the rationale for risk ratings presented earlier in the document, the risk of contact between pack goats and bighorn sheep under this alternative would be therefore be “low.”

Other mitigation measures would help decrease the potential for disease transmission between pack goats and bighorn sheep, even if contact between the two were to occur. Reporting of any observed contact between pack goats and bighorn sheep would not help

prevent disease transmission, but it may facilitate determination of whether disease transmission occured and promote a rapid management response. Requiring veterinary health inspection and disease testing of pack goats and handler possession of a health certificate for each pack goat entering the Forest would help limit the risk of disease transmission if contact with bighorn sheep were to occur. A veterinary inspection would detect disease in animals showing symptoms of respiratory disease or other infectious conditions such as pink eye and sore mouth. Disease testing using approved protocols could be conducted for pathogens commonly implicated in bighorn die-offs to identify potentially infectious but non-symptomatic animals. However, implementation of this requirement could be difficult. Veterinarians commonly conduct health inspections and disease testing for a variety of domestic animals using standardized protocols to conform to various state or federal regulations. However, disease testing of pack goats would involve specific sampling protocols for a suite of potential pathogens (H. Edwards, WGFD, personal communication 04/20/2017). There is currently a protocol available for pack goat users to test their animals for *M. ovipneumoniae* through the Washington Animal Disease Diagnostic Lab (see https://waddl.vetmed.wsu.edu/), but similar protocols available to pack goat users have not been established for other pathogens of concern. Additionally, there is concern over the efficacy of testing because disease-causing bacteria may be carried by animals that are not shedding them, and testing may not detect the disease in such animals. These same animals may begin shedding the bacteria at a later time, especially if they are subjected to stress (P. Klein, U.S Forest Service, personal communication, 10/2/2017), and could then potentially transmit pathogens to bighorn sheep. There is also the possibility that "certified" animals could come into contact with other livestock after being tested and inspected, and potentially contract pathogens that could be transmitted to bighorn sheep.

To be effective, these measures would depend on the diligence of the pack goat user. Many pack goat users have stated their willingness to comply with any mitigation measures needed to limit the potential for disease transmission from their animals to bighorn sheep. However, some pack goat users have stated that "the restrictive nature of these best management practices will act as a deterrent for those users not willing to submit to the extensive preparation and implementation of these practices" (Jennings 2011). This indicates that some pack goat users will perceive mitigation measures as restrictive and difficult to implement, and that if they deter some users others may simply choose not to comply. Some level of non-compliance would be expected. Compliance checks by the Forest Service would be infrequent due to the very remote and rugged environments that goat packing takes place in.

The overall potential for disease transmission between pack goats and bighorn sheep if contact were to occur would be lower compared to a scenario where pack goat use was allowed but these mitigation measures were not used. However, these mitigation measures have not been implemented on the SNF or elsewhere, and there is uncertainty about their ultimate efficacy. As a result, there would still be substantial uncertainty associated with the potential for disease transmission to occur resulting in a bighorn sheep pneumonia die-off.

Summary

A long history of large-scale, all-age die-offs in bighorn sheep due to pneumonia exists across North America. The causal agents and mechanisms that lead to pneumonia outbreaks in bighorn sheep have been the subject of much research and the body of knowledge has

advanced considerably, but there continues to be significant uncertainty and scientific debate on this topic.

Not all bighorn sheep disease events can be attributed to contact with domestic sheep or goats. However, there is extensive scientific literature supporting the relationship between disease in bighorn sheep populations and contact with domestic sheep. The literature documents both circumstantial evidence linking bighorn die-offs in the wild to contact with domestic sheep, and controlled experiments where healthy bighorn sheep exposed to domestic sheep resulted in bighorn sheep mortality. Recent serological research has documented the transmission of specific pathogens between domestic and bighorn sheep that are non-lethal in domestic sheep, but lethal in bighorn sheep.

The literature is much less developed for domestic goats, there is very little research specific to pack goats, and scientific uncertainty remains on the potential for disease transmission from domestic goats and pack goats to bighorn sheep. It has been established that domestic goats can carry the bacteria that have been identified as playing a primary role in the development of pneumonia in bighorn sheep, and examples were cited earlier in this document where there is evidence for domestic goats transmitting disease to bighorn sheep. However, there is also evidence that domestic goats, and pack goats in particular, present a lower risk of disease transmission to bighorn sheep that could result in catastrophic all age die-offs. Evidence is emerging to suggest that pack goats have a low prevalence of at least one of the primary pathogens involved in the development of pneumonia in bighorn sheep (*Mycoplasma ovipneumoniae)*, and that pathogens transmitted from domestic goats are often less virulent to bighorn sheep than those transmitted by domestic sheep. However, numerous questions remain unresolved regarding the overall potential for disease transmission risk from pack goats to bighorn sheep.

Population characteristics of bighorn sheep herds on the SNF were summarized above. The SNF provides habitat for six of Wyoming's eight core native herds which comprise about 75% of the state's bighorn sheep population. Domestic sheep grazing and pack goat use on the SNF relative to these herds were then described, and the risk of contact and potential for disease transmission between domestic sheep and bighorn sheep, and pack goats and bighorn sheep, was assessed. Because there is very little domestic sheep grazing on the SNF, and none occurs within proximity to core native bighorn sheep herds, domestic sheep grazing on the Forest presents little risk to bighorn sheep. Without restrictions on pack goat use, there would be spatial and temporal overlap between pack goat use and core native bighorn sheep herds. Characteristics of pack goat use were described that would moderate the risk of contact between pack goats and bighorn, as well as the risk of disease transmission if contact were to occur. The risk of disease transmission was characterized as relatively low, but the uncertainty associated with this risk was also recognized.

Management scenarios where pack goat use was prohibited, or allowed with required mitigation measures, were also evaluated. If pack goat use were prohibited, there would be essentially no risk and uncertainty. If pack goats were allowed with required mitigation measures, the risk of contact between pack goats and bighorn sheep along with the risk of disease transmission would be further reduced compared to a scenario where they were allowed with no required mitigation. The analysis pointed out that it is unknown how effective the mitigation measures would be since they have not been implemented on the SNF or elsewhere.

Cumulative Effects

The SNF is working with other State, Federal, and local partners (State-wide Bighorn Sheep/Domestic Sheep Interaction Working Group) to better identify where bighorn sheep occur, where they wander, and how they might interact with other herds and domestics. This effort is expected to help reduce potential cumulative effects to bighorn sheep on the SNF.

Four of the six core native herds on the SNF are potentially within 35 km of domestic sheep that are on lands adjacent to the Forest (Table 3). The closest potential domestic sheep/goat grazing on public lands to the Trout Peak herd is about 19 km (12 miles) east on Bureau of Land Management lands. The closest potential domestic sheep/goat grazing on public lands to the Wapiti Ridge herd is about 29 km (18 miles) east on Bureau of Land Management lands. The closest potential domestic sheep/goat grazing on public lands to the Younts Peak herd is about 42 km (26 miles) east on Bureau of Land Management lands (Table 3). However, those potential sheep grazing sites are separated from these herds by miles of unsuitable bighorn sheep habitat as well as by Highway 120 (McWhirter, WGFD, pers. comm. 2017), and therefore the concern for disease transmission to bighorn sheep in these areas is lower.

Domestic sheep grazing on adjacent lands is more of a concern for the Clarks Fork and Francs Peak herds. The closest domestic sheep/goat grazing to the Clarks Fork herd is about 2 km (1 mile) east on private lands. Recently domestic sheep grazing has occurred on private lands in Owl Creek within habitat of the Francs Peak herd. However, the Wyoming Wild Sheep Foundation and the individual landowner in question have recently cooperated to develop water sources at lower elevations (33 km from occupied sheep habitat) to reduce the need to graze domestic sheep in closer proximity to occupied bighorn sheep habitat (McWhirter, WGFD, pers. comm. 2017) which should help reduce disease transmission risk.

In the recent past, the closest domestic sheep grazing on public lands to the Whiskey Mountain herd was about 10 km (6 miles) west on the BTNF. However, those allotments were recently closed to sheep grazing (USDA Forest Service 2017b). As a result, no known domestic sheep grazing occurs within 35 km of this herd, either on the SNF or BTNFs. The closest domestic sheep grazing on lands outside of the SNF to this herd is now more than 60 km away on the BTNF. There have not been any active domestic sheep or goat grazing allotments on the Wind River Reservation within this herd's home range for at least several decades, and there are no known small hobby or farm flocks of domestic sheep or goats (P. Hnilica, U.S. Fish & Wildlife Service, personal communication 10/2/2017). There are no domestic sheep or goat grazing allotments on the Wind River Reservation within the Temple Peak bighorn sheep herd's range. There has been a small hobby flock of domestic sheep on the North Fork Popo Agie River near the Wind River Reservation boundary in the recent past, and a small flock of domestic sheep at low elevation on the Wind River Reservation along Trout Creek whose current status is unknown (P. Hnilica, U.S. Fish & Wildlife Service, personal communication 10/2/2017).

Pack goat use would still occur within occupied habitat for Whiskey Mountain bighorn sheep on adjacent BTNF lands, and there would be some risk of contact and disease transmission from pack goats to bighorn sheep as a result.

The potential presence of domestic sheep on lands outside the jurisdiction of the SNF, yet still within the 35 km foray distance of bighorn sheep, adds to the risk of contact between bighorn sheep on the Forest and domestic sheep. Such incidents originating from lands

adjacent to, but outside the jurisdiction of, the SNF increase the likelihood of contact with domestic sheep and increase the risk of disease transmission to these herds.

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Appendix A. Shoshone Forest Order 16-003

Order Number 16-003

UNITED STATES DEPARTMENT OF AGRICULTURE
U.S. FOREST SERVICE
SHOSHONE NATIONAL FOREST
FOREST ORDER

Pursuant to 36 C.F.R. § 261.50(a), the following acts are prohibited on the Shoshone National Forest:

Possession or use of domestic goats on any National Forest System lands on the Wapiti, Clarks Fork, Greybull and Wind River Ranger Districts as shown on the attached map.

PROHIBITIONS:

1. Possession or use of domestic goats in special closure area. 36 C.F.R. § 261.53(a) and 36 C.F.R. § 261.58(s).

EXEMPTIONS: Pursuant to **36 CFR 261.50(e)** the following persons are exempt:

(1) Persons with a Forest Service permit specifically authorizing the otherwise prohibited act or omission.

(2) Any Federal, State or local officer, or member of an organized rescue or firefighting force engaged in the performance of an official duty.

(3) Forest Service contractors or permittees engaged solely in the performances of official permit or contract obligations.

AREA DESCRIBED: National Forest System lands as depicted on Exhibit A.

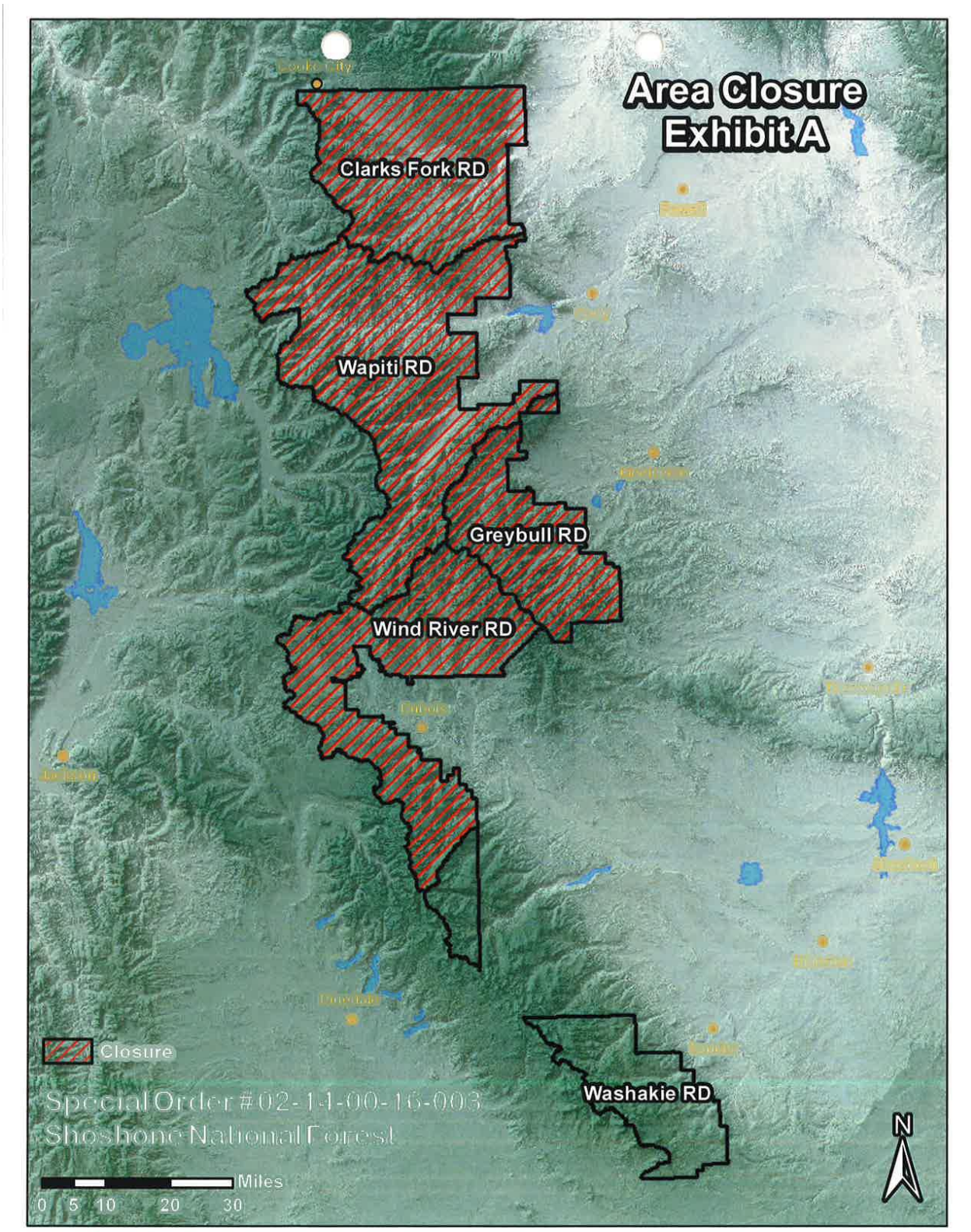
PURPOSE: The purpose of this Order is to protect the health and viability of bighorn sheep, a Region 2 sensitive species, on their core habitat, until a thorough risk assessment can be completed.

IMPLEMENTATION: This Order will be in effect on June 24, 2016 and shall remain in effect until rescinded, until December 31, 2019, whichever event occurs first.

Done at Cody, Wyoming, this 24th day of June 2016.

Joseph G. Alexander
Forest Supervisor
Shoshone National Forest

Any violation of this Order is punishable as a Class B misdemeanor by a fine of not more than $5,000 for an individual or $10,000 for an organization or imprisonment for not more than six (6) months, or both. [Title 16 USC 551, Title 18 USC 3571 (b)(6), Title 18 USC 3581 (b)(7)].


Area Closure
Exhibit A
Clarks Fork RD
Wapiti RD
Greybull RD
Wind River RD
Washakie RD
Closure
Special Order #02-14-00-16-003
Shoshone National Forest
Miles
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